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A comprehensive analysis of human Pre-Ta LINE-1 and Ya-lineage Alu mobile elements

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A COMPREHENSIVE ANALYSIS OF HUMAN PRE-Ta LINE-1 AND Ya-LINEAGE *ALU* MOBILE ELEMENTS

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DEDICATION

This work is dedicated to the Glory of God and in loving memory of my late grandmother Agnetta Odongo *Nya gi Kola* and my late beloved sister Agnetta Odongo. *Dani*, you taught me the importance of hard work, the reward of selfless giving and the power of a life devoted to God.Proverbs 31:10-31 so patently embodies your enduring spirit. “Many daughters have done virtuously, nobly and well (with the strength of character that is steadfast in goodness), but you excel them all”. These tenets of your life changed me and I will carry them for the balance of my years. Netta, you helped us dig deep and find strength we thought we never had. It seems like you lived your life like a candle in the wind. Your candle burned out long before your legend ever will and we are better people because of you. Your strength and longsuffering remain beacons for us as we walk into the future.

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ABSTRACT

Long INterspersed Elements (LINEs or L1) and Short INterspersed Elements (SINEs) have played a critical role in shaping the human genomic landscape, making up about 33% of the human genomic mass. In this work, preTa, an L1 subfamily and the Ya-lineage of Alu SINEs were examined to determine their impact on the human genomic architecture and diversity. We analyzed 362 preTa L1 elements and 2318 Ya lineage Alu elements using computational methods and polymerase chain reaction (PCR) assays. PCR analysis on a geographically distinct panel of human populations indicated that 33 (14%) of preTa L1 elements and 313 (22%) of Ya-lineage Alu elements were polymorphic for insertion presence/absence. DNA sequence analysis of the preTa and the Ya-lineage subfamilies indicated an estimated average age of 2.34 and 2.27 million years respectively. This suggests that these elements began to amplify after the human lineage radiated from the non-human primates. None of the mobile elements analyzed were also located in orthologous non-human primate loci, supporting the fact that they are homoplasy free genetic characters. The continued amplification of mobile elements throughout evolutionary time and their variable insertion frequencies in diverse human populations make them robust tools for population genetics and comparative genomics.

CHAPTER ONE:

BACKGROUND

The concept of transposons or mobile DNA in living organisms was first reported by Barbara McClintock in 1944 and in the years following. The concept involved the initial identification and characterization of Ac/Ds (Activator/Dissociation) elements involved in the breakage-fusion-bridge cycle (Comfort 1999; Comfort 2001; McClintock 1956) that cause the variegated color patterns in kernels of maize. Her depiction of the phenomenon directly involved gross chromosome rearrangements mediated by transposable elements marked the onset of transposon research. These elements consist of linear DNA segments that either move from one genomic location to another, or make copies of themselves, with the copies inserting in a new genomic locations. There are two main classes of mobile elements depending on whether their amplification occurs via an RNA or DNA intermediate: Retrotransposons and DNA transposons, respectively.

DNA transposons have inverted terminal repeats and encode transposase activity. They generally move through a “cut and paste” mechanism utilizing their transposase to excise themselves from one location in the genome and insert themselves in a different genomic location (Mizuuchi 1992; Smit and Riggs 1996; van Luenen et al. 1994). They constitute about 3% of the human genome, though it is unlikely they remain transpositionally active because they are fossils of ancient elements (Lander et al. 2001).

Retrotransposons, on the other hand amplify by a “copy and paste” mechanism which involves an RNA intermediate (Weiner et al. 1986). The original retrotransposon is maintained *in situ* where it is transcribed. The transcript is then reverse transcribed into a cDNA copy that integrates into a new genomic location (Luan et al. 1993; Whitcomb and Hughes 1992). Approximately 45% of the human genome is composed of retrotransposons (Lander et al. 2001),

and, although the overwhelming majority are inactive, a small number retain the ability to retrotranspose (Brouha et al. 2003; Cordaux et al. 2004; Sassaman et al. 1997).

Retrotransposable elements can be classified as either autonomous or non-autonomous. Autonomous elements encode certain proteins necessary for their amplification. There are two classes of autonomous retroptransposons: LTR (Long Terminal Repeat) retrotransposons and non-LTR retrotransposons. The structure of LTR retrotransposons is similar to retroviruses, but they lack a functional envelope (*env*) gene, which prevents them from moving from cell to cell (Flavell et al. 1997). They also lack the genomic components required for making a functional viral capsule. They have transcriptional regulatory sequences located in the flanking LTRs, and several open reading frames (ORFs) that are responsible for their amplification. These proteins include endonuclease for cleaving the insertion site and reverse transcriptase to copy RNA into DNA. There are some non-autonomous LTRs which have partially or fully deleted coding capacity, and they are inactive pseudogenes representing ancient retrotranspositional events. Some are, however, able to utilize *trans*-acting factors from autonomous elements to efficiently amplify themselves (Curcio and Garfinkel 1994). The LTR retrotransposons include elements such as mouse intracisternal A-particles (IAPs) (Kuff and Lueders 1988) and Human endogenous retroviruses (HERVs) (Benit et al. 1999). About 8% of the human genome is composed of defective endogenous retroviruses and solitary LTRs derived from recombination between the 5' LTR and the 3' LTR of these elements (Lander et al. 2001).

The non-LTR retrotransposon class contains LINEs (Long INterspersed Elements) that includes inactive elements, such as L2 in humans, and active elements, such as L1 in humans and mice (Lander et al. 2001; Malik et al. 1999; Smit 1999). These elements utilize internal promoter sequences located in the 5' end of their coding sequence and they make polyadenylated RNA.

They differ from traditional mRNAs in that they generally make a bicistronic RNA that codes for both an RNA binding protein (ORF1) and an ORF2 protein with dual endonuclease and reverse transcriptase activities (Kazazian 2000). The sites for priming reverse transcription are located near the 3' end of the RNA, and are commonly provided by the 3' poly A tail of the mRNA.

In addition, there are several other classes of non-autonomous retrotransposons found in mammalian genomes. These elements do not encode any proteins and therefore require activities encoded by other autonomous retroposons for their ability to amplify. The most abundant of these are the SINES (Short INterspersed Elements). These SINES are small elements, usually 90 to 300 bp in length, that are transcribed by RNA polymerase III. These elements are derived either from tRNA genes (Daniels and Deininger 1985) or from the 7SL RNA gene (Ullu and Tschudi 1984). Several lines of evidence suggest that SINES rely on LINES for their amplification. It has been shown that the 3' end of SINES show strong sequence identity with the 3' ends of LINES (Okada and Hamada 1997; Weiner et al. 1986). It is thought that SINES may have arisen by a fusion of a tRNA related sequence with the 3' end of an existing LINE, resulting in the ability of the LINES to complement amplification of the SINES. LINES are also similar to SINES in that they share direct repeats of varying lengths (Daniels and Deininger 1985). Analyses of the direct repeats show that they not only share the same consensus sequence (Jurka 1997), but that the endonuclease associated with the LINE elements preferentially cleaves at that consensus (Feng et al. 1996). The most prominent members of the SINES are Alu elements in humans (Batzer and Deininger 2002), and their B1 counterparts in mice (Vassetzky et al. 2003). Alu elements have multiplied in copy number to over a million members in the haploid genome and account for about 11% of the mass of the human genome (Batzer and Deininger 2002; Lander et al. 2001).

Other non-autonomous retrotransposons in the human genome include processed pseudogenes (Esnault et al. 2000) and SVA elements (Ostertag et al. 2003). Processed pseudogenes were first described as DNA elements structurally colinear with gene mRNA, lacking promoters, introns, and, in general without protein coding capacity due to mutations and frequent stop codons (Pavlicek et al. 2002). Their mRNA-derived structure, poly A tails at the 3' end, and the presence of direct repeats of variable length led to the hypothesis that their formation requires reverse transcriptase (Tchenio et al. 1993; Vanin 1985; Weiner et al. 1986). The estimated portion of processed pseudogenes in the human genome is ~0.5% (Dunham et al. 1999), with an estimated copy number of 23000-33000 (Goncalves et al. 2000). Few cases of expressed, intronless genes with a likely retrotranspositional origin (retrogenes) have been described in several organisms (Betran et al. 2002; Brosius 1999; Lahn and Page 1999). SVA elements are composite retroposons made up of a SINE-R (derived from human endogenous retrovirus, HERV-K10), a VNTR (Variable-Number-of-Tandem-Repeats) and an *Alu*-like sequence (Shen et al. 1994). SVA insertions contain the hallmarks of retrotransposition in *trans* by LINE elements. They are flanked by L1-like TSDs, they end in poly A tails, they can transduce 3' sequence and they occasionally truncate and invert during insertion. It is highly likely, therefore that these elements borrow L1 proteins for their amplification. SVA elements along with Alu elements have been shown to be the only non-autonomous retrotransposons that cause diseases in humans.

Thus, transposable elements and transposon derived sequences make up about 45% of the total mass of the human genome and have played a key role in the shaping of human and other eukaryotic genomes.

Alus and LINEs

Alu elements are the major SINE family in primate genomes, having amplified to a copy number of over one million during the past 65 million years (Batzer and Deininger 2002; Smit 1996). Alu elements were identified initially as a component of human DNA renaturation curves (Schmid and Deininger 1975). Full length Alu elements are 300 bp long, are dimeric in structure and are ancestrally derived from the 7SL RNA gene, which forms part of the signal recognition particle (Rubin et al. 1980; Ullu and Tschudi 1984). Their dimeric structure and middle A rich region can be traced back to an initial gene duplication early in primate evolution (Deininger and Batzer 1993; Shedlock and Okada 2000). The highly successful amplification of Alu elements, despite being non-autonomous, is a sign of how efficiently they have commandeered the L1 retrotransposition machinery for purposes of their own propagation (Batzer and Deininger 2002).

Despite the high numbers of Alus in the human genome, only a small number are retropositionally competent (Cordaux et al. 2004). Over the 45-60 million years that Alus have amplified, the few active "master" or "source" genes have accumulated mutations which are inherited by their copies. The result is that the Alu family is composed of several distinct subfamilies of different genetic ages forming a hierarchical series (Deininger et al. 1992; Leeflang et al. 1993; Leeflang et al. 1992). The older elements have accumulated a large number of random mutations over evolutionary time. They therefore have fewer diagnostic mutations as compared to the younger elements.

Although the peak of Alu amplification was ~40 million years ago, several young subfamilies have been identified, many of which are still active and generate *de novo* insertions. An overwhelming majority of the recently integrated human Alu elements belong to one of several closely related "young" Alu subfamilies, known as Yc1, Yc2, Ya5, Ya5a2, Ya8, Yb8,

Yb9 (Batzer et al. 1990; Batzer et al. 1995; Carroll et al. 2001; Carter et al 2004; Matera et al. 1990; Otieno et al. 2004; Roy et al. 1999; Roy-Engel et al. 2001). These “young” Alu elements are largely human specific and are very rarely found in orthologous loci in the genomes of non-human primates. Some of these “young” Alu elements have amplified so recently that they are polymorphic in respect to their presence or absence in a variety of human populations (Batzer and Deininger 1991). The *de novo* insertions by these Alus is responsible for approximately 0.1% of human genetic diseases through unequal homologous recombination that cause genomic duplications and deletions (Deininger and Batzer 1999).

Alu elements have also been found at the junctions of segmental duplications (Bailey et al. 2003) and it is thought that Alu-Alu recombination is responsible for the expansion of these duplications. These duplications have caused the shuffling of exons and the evolution of new proteins. Alu elements have also been found in exons and it has been established that these Alu-containing exons are predominantly, if not exclusively alternatively spliced (Lev-Maor et al. 2003; Sorek et al. 2002). Alu elements cause alternative splicing by either landing in splice junctions or activating cryptic splice sites.

Long INterspersed Elements (LINEs) are the other predominant mobile element family found in the human genome (Singer 1982; Singer et al. 1983). LINE elements are the master retrotransposons in mammalian genomes. Besides duplicating themselves, it has been established that they have been responsible for the genomic expansion of non-autonomous retrotransposons which include Alu elements, processed pseudogenes, and SVA elements in the human genome. Over evolutionary time, these elements have acquired a number of roles, some of which are useful, while others have been shown to be detrimental.

In mammals, the overwhelming majority of LINE retrotransposons are inactive, defective elements, owing to 5' truncation, inversion, and point mutations. Full length LINE elements are roughly 6000 base pairs (bp) in length. The consensus sequence revealed that LINE elements have a 5' untranslated region (UTR) with internal RNA polymerase II promoter activity (Prak and Kazazian 2000; Swergold 1990). It also contains two open reading frames (ORFs) both of which are vital in the amplification process (Fanning and Singer 1987; Moran et al. 1996; Singer et al. 1993). The first ORF encodes an approximately 40-kDa protein (p40) with RNA binding activity but no known physiological function (Hohjoh and Singer 1997; Kolosha and Martin 1997; Martin and Bushman 2001). The second ORF encodes an approximately 150-kDa protein with three conserved domains, an NH2-terminal endonuclease (EN) domain (Feng et al. 1996), a central reverse transcriptase (RT) domain (Mathias et al. 1991), and a COOH-terminal zinc knuckle-like domain (Fanning and Singer 1987). The LINE EN domain cleaves one strand of a double stranded DNA at genomic sites characterized by the loose consensus sequence AA/TTTT (Cost and Boeke 1998; Feng et al. 1996; Jurka 1997). In addition, LINEs have a 3' UTR that ends in an AATAAA polyadenylation signal, and a polyA tail. The youngest class of LINE elements are LINE-1 or L1 elements which are believed to have started amplifying around the time of the mammalian radiation about 120 million years ago (Pascale et al. 1990; Smit 1996). These L1 elements have amplified to a copy number of 500,000 in the haploid human genome (Lander et al. 2001). An estimated 1000-1500 of L1 elements in the human genome are human-specific (Myers et al 2002; Salem et al. 2003) with ~320 of these belonging to the preTa subfamily (Salem et al 2003). An estimated 40-60 L1 elements are active, full length and capable of retrotransposition (Brouha et al. 2003; Myers et al. 2002; Prak and Kazazian 2000).

L1 elements are likely reverse transcribed and integrated into the genome by a coupled reverse transcription/integration process called target primed reverse transcription (TPRT) (Luan et al. 1993). The endonuclease domain of ORF2 cleaves the noncoding strand of its target site, freeing a short oligonucleotide with a 3'-OH. Reverse transcriptase then uses this oligonucleotide as a primer and the L1 RNA as a template for the reverse transcription reaction. This is followed by cleavage of the coding strand and integration. This process is completed by a second strand DNA synthesis, ligation, and filling in of genomic sequence flanking the L1. TPRT produces a perfect duplication of the original target site that serves as an important landmark defining the boundaries of newly integrated elements (Fanning and Singer 1987). The vast majority of L1 insertions are highly truncated at the 5' end such that the average insertion is about 1kb long (Lander et al. 2001). This is due to the lack of processivity of reverse transcriptase. Truncation may also be due to cellular RNAse H competing with L1 reverse transcriptase.

Approximately 25% of recent L1 insertions also contain an inversion of a few hundred to fifteen hundred nucleotides of L1 sequence. This inversion involves the 5' terminal end of the L1 element and is 5' truncated itself. The point of inversion may contain a deletion, a duplication or neither. Inversion is caused by a second internal priming event before TPRT is completed and is called twin priming (Ostertag and Kazazian 2001).

The amplification of L1 elements has had a major impact on the human genome. The net effect of these insertions has been the structural remodeling of the human genome. L1 elements have greatly increased the size of the human genome through their own amplification and by providing the necessary machinery for the amplification of other mobile elements like Alu repeats (Esnault et al. 2000; Jurka 1997; Kajikawa and Okada 2002). L1 elements have also been shown to cause disease in humans (Burwinkel and Kilimann 1998; Kazazian et al. 1988; Segal et

al. 1999). They do this through insertion into genes, providing the machinery for the insertion of other retrotransposons into genes, and by inserting within splice junctions and regulatory regions. This results in exon skipping, decreased transcription, or decreased stability of the primary transcript. Because of inconsistency of polyA signals during transcription, unique genomic sequences flanking the 3' ends of L1s may be carried along in the retrotransposition event (Goodier et al. 2000; Hughes and Coffin 2001; Moran et al. 1999; Pickeral et al. 2000). This event can cause exon shuffling which could potentially create new genes. L1 elements provide sequence homology and this makes them extremely recombinogenic leading to genomic duplications and deletions (Gilbert et al. 2002; Hughes and Coffin 2001). L1 elements have also been proposed to play a role in X Chromosome inactivation (Lyon 1998; Lyon 2000) as well as the repair of double stranded DNA breaks especially where the L1 insertion is not bracketed by perfect target site duplications (Morrish et al. 2002).

Alu and L1 elements have also been utilized as genetic systems for the study of population genetics and phylogenetic relationships. Mobile elements are unique genetic systems because of their continuous propagation (Nikaido et al. 1999; Santos et al. 2000; Shedlock and Okada 2000; Shimamura et al. 1997). Alu and L1 elements are both identical by descent with known ancestral states, which means that individuals who share an insertion likely inherited it from a common ancestor (Batzer et al. 1994). By virtue of the homoplasy-free nature of these elements, they are a rich source of population specific genetic variation that can be used in population genetics (Batzer and Deininger 2002; Roy-Engel et al. 2001). L1 elements show promise as future gene delivery vectors due to their stability and ability to transduce 3' sequences (Soifa et al. 2001).

Here, we report a comprehensive analysis of the genomic impact of L1 pre-Ta and Alu Ya5 subfamily on human genomic structure and genetic diversity. Using computational approaches,

we queried the draft sequence of the human genome for sequences containing distinct diagnostic mutations representing these two subfamilies. We then stripped the entire draft human genomic sequence of these elements, designed unique sequence oligonucleotide primers and subjected each element to polymerase chain reaction (PCR) analysis using a subset of four geographically distinct human populations and several non-human primates. Based on these analyses, we determined mobile element age estimates, genomic diversity, phylogenetic origin and the levels of polymorphism among the geographically distinct populations. We also identified and characterized the transduction of unique genomic DNA sequences carried at the 3' end of some pre-Ta L1 insertions. We have also identified paralogous insertions as well as insertions in orthologous loci in non-human primates and determined the underlying mechanisms that generated them. As a result, we were able to shed light on the amplification dynamics, stability, and the role that these mobile elements have played in the evolution of the human genome (Otieno et al. 2004; Salem et al. 2003). We identified and characterized 2400 Alu Ya5 and 340 pre-Ta LINE elements. These new insertions have been found to be homoplasy free and will provide powerful genomic tools for primate comparative genomics and human population genetics.

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CHAPTER TWO:

LINE-1 PRE Ta ELEMENTS IN THE HUMAN GENOME*

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Introduction

Computational analysis of the draft sequence of the human genome indicates that repetitive sequences comprise 45-50% of the human genome mass, 17% of which consists of Long INterspersed Elements (LINE-1s or L1s) (Lander et al. 2001; Prak and Kazazian 2000; Smit 1999). L1 elements are restricted to mammals, having expanded as a repeated DNA sequence family over the last 150 million years (Smit et al. 1995). Full-length L1 elements are approximately 6 kilobases (kb) long and propagate via an RNA intermediate in a process known as retrotransposition. L1 integration likely occurs by a mechanism termed target primed reverse transcription (TPRT) (Luan et al. 1993). This mechanism of mobilization provides two useful landmarks for the identification of young L1 inserts: an endonuclease related cleavage site (Cost and Boeke 1998; Cost et al. 2001; Jurka 1997) and direct repeats or target site duplications flanking newly integrated elements (Fanning and Singer 1987).

L1 retrotransposons have had a significant impact on the human genome through a variety of different mechanisms. *De novo* insertions disrupting open reading frames and splice sites have resulted in a number of human diseases (Deininger and Batzer 1999; Kazazian 1998; Kazazian et al. 1988), new L1 integrations have been shown to have the potential to alter gene expression (Rothbarth et al. 2001; Yang et al. 1998), and once in the genome L1 elements provide regions of sequence identity blanketing the genome, that can be exploited during recombination (Fitch et al. 1991). L1 elements also generate sequence duplications by transducing adjacent genomic sequences at their 3' end, thereby "shuffling" genomic sequence (Boeke and Pickeral 1999; Goodier et al. 2000; Moran et al. 1999). More recently, it has been suggested that L1 elements have paradoxical roles in genomic stability by serving both as molecular band aids, repairing double stranded breaks in mammalian cells and as suspects for the

generation of genomic deletions in (Gilbert et al. 2002; Kazazian and Goodier 2002; Symer et al. 2002). Thus, L1 elements exert a significant influence on the architecture of the human genome and provide dynamic units capable of ongoing change within the human genome.

As a result of the limited amplification potential of the diverse L1 gene family, a series of discrete L1 subfamilies exist within the human genome (Deininger et al. 1992; Smit et al. 1995). L1 elements have expanded at different times during primate evolution producing subfamilies of various ages (Deininger et al. 1992; Smit et al. 1995). Depending on the amplification period of the L1 subfamily, some L1 elements may be unique to a single phylogenetic lineage, species, or even a single population. Such is the case with the L1Hs (Human specific) Ta (transcribed, subset a) (Skowronski et al. 1988) subfamily, which has been shown to be present only in the human lineage (Myers et al. 2002).

Even though there are approximately 500,000 L1 elements in the human genome only a limited subset of 30-60 L1 elements appear to be capable of retrotransposition (Moran et al. 1996; Sassaman et al. 1997). *De novo* L1 insertions resulting human disease are largely product of L1Hs Ta integrations, which has been shown to be youngest most active L1 subfamily found in the human genome (Boissinot et al. 2000; Myers et al. 2002; Sheen et al. 2000). However, at least one L1 insert (JH-28) in exon 14 of the factor VIII gene resulting in hemophilia A, was the result of a preTa insertion, providing the first proof that preTa L1 elements are also currently capable of retrotransposition (Kazazian et al. 1988). Previous studies have shown that some members of the preTa L1 subfamily have inserted so recently in the human genome that they are polymorphic with respect to insertion presence/absence (Boissinot et al. 2000; Ovchinnikov et al. 2002), all of which makes preTa L1 elements a likely source of identical-by-descent mobile element based variation for the study of human population genetics.

Members of L1 preTa subfamily share a common three base pair diagnostic sequence within the 3' untranslated region (UTR), which separates them from the other L1 subfamilies. As the name suggests, the preTa L1 subfamily is believed to predate the amplification of the L1Hs Ta subfamily in the human lineage. However, the phylogenetic origin and level of human genetic diversity associated with preTa L1 elements remains largely undefined. The following work provides a comprehensive analysis of the preTa L1 subfamily from the draft sequence of the human genome.

Results

L1 preTa Subfamily Copy Number

To identify recently integrated preTa subfamily L1 elements from the human genome, the draft sequence of the human genome (database version: BLASTN 2.2.1 [Apr-13-2001]) was searched using the Basic Local Alignment Search Tool (BLAST) (Altschul et al. 1990) with an oligonucleotide sequence that is complementary to a highly conserved motif in the 3' untranslated region (UTR) of preTa L1 elements. This 19 base pair (bp) query sequence (CCTAATGCTAGATGACACG) includes the preTa subfamily-specific diagnostic mutation "ACG" at its 3' end (position 5930-5932 relative to LRE-1) (Dombroski et al. 1991). Three hundred sixty two unique L1 preTa LINE elements from 2.868 $x10^9$ bp of available human draft sequence. Extrapolating this number to the actual size of the human genome (3.162 $x10^9$ bp), we estimate that this subfamily contains about 400 elements. Taken with the estimate from the L1Hs Ta data (Myers et al. 2002), we estimate that there are over 900 human specific LINE-1 elements in the human genome. Of the 362 L1 preTa elements retrieved, 6 resided at the end of sequence contigs and were not amenable to additional analysis. One hundred five (29%) of the 356 (362-6) remaining elements were essentially full length, and 251 were truncated to variable

lengths. Alignment and sequence analysis of the full-length elements revealed that 29 contained two intact open reading frames and therefore may be capable of retrotransposition. The complete data set is available at the Batzer lab of Comparative Genomics website (http://batzerlab.lsu.edu) under publications.

Estimated Subfamily Age

The average ages of L1 elements can be determined by the level of sequence divergence from the subfamily consensus sequence using a neutral mutation rate for primate non-coding sequence of 0.15% per million years (Miyamoto et al. 1987). The mutation rate is known to be about 10 times greater for CpG bases as compared to non-CpG bases as result of the spontaneous deamination of 5-methyl cytosine (Bird 1980). Thus, two age estimates based upon CpG and non-CpG mutations can be calculated for the preTa subfamily of L1 elements. A total of 74,048 bases from the 3' UTR of 356 preTa L1 elements were analyzed. Three hundred sixty-one total nucleotide substitutions were observed. Of these, 303 were classified as non-CpG mutations against the backdrop of 71,912 total non-CpG bases, producing a non-CpG mutation density of 0.004213 (303/71,912). Based upon the non-CpG mutation density and a neutral rate of evolution (0.004213/0.0015) the average age of the L1 preTa LINE-1 elements was 2.81 million years old. A total of 58 CpG mutations out of 2,136 total CpG nucleotides were found across the same 356 LINE elements, yielding a CpG based mutation density of 0.027154 (58/2,136). With the expectation that the CpG mutation rate is about 10 fold higher than the non-CpG mutation rate, the approximate age of the L1 preTa subfamily using the CpG mutation density is 1.86 million years old. These estimates are in good agreement with one another and taken together, these estimates produce an average age of 2.34 million years old, which is in good agreement with the idea that the preTa L1 subfamily is evolutionarily older than the L1Hs Ta subfamily

(estimated average age 1.99 million years) (Boissinot et al. 2000; Myers et al. 2002). In addition the average age estimates reported here provide a relative time frame by which to compare L1 retrotransposition activity, and should not be confused with the age of origin.

Similar to the L1Hs Ta subfamily, the L1 preTa subfamily can also be grouped into two subgroups, ACG/A and ACG/G, based on an "A" or "G" base at position 6015 relative to L1.2 (Accession number M80343). In order to determine the relative ages of each subgroup, we analyzed the level of sequence divergence in each subgroup. The ACG/A subgroup contained 127 total nucleotide substitutions with 98 of these classified as non-CpG mutations against the backdrop of 20,402 total non-CpG bases. This yields a non-CpG mutation density of 0.004803 (98/20,402) and produces an estimated age of 3.20 million years old. Twenty nine of 127 total mutations were classified as CpG mutations against a backdrop of 606 CpG total bases, which yields a CpG mutation density of 0.047855 (29/606) producing an estimated age of 3.28 million years. The ACG/G subgroup contained 221 total nucleotide substitutions with 191 of these classified as non-CpG mutations against the backdrop of 51,106 total non-CpG bases, which yields a non-CpG mutation density of 0.003737 (191/51,106), producing an estimated age of 2.49 million years old. Thirty of 121 total mutations were classified as CpG mutations against a backdrop of 1518 CpG total bases, which yields a CpG mutation density of 0.019763 (30/1518) producing an estimated age of 1.35 million years. We calculated the average age of each subgroup as 1.92 and 3.24 million years for the ACG/G and ACG/A respectively. Although it is likely that the L1Hs Ta subfamily is derived from one of the preTa L1 subsets based on the estimated ages of these L1 subfamilies the transition intermediates between preTa and Ta subfamilies are not clear.

Features of L1 preTa Integration Sites

One hallmark of L1 integration is the generation of target site duplications flanking newly integrated elements. Two thousand bases of flanking sequence on each side of the element were searched for target site duplications. Clear target site duplications are considered to be target site duplications at least 10 bases in length. Of the 356 elements analyzed, we were able to identify clear target site duplications for 252 elements. We then determined the L1 integration sites for these 252 L1 preTa insertions with clear target duplications. A complete list of L1 integration sites is shown in Table 1, and further supports the notion that some integration sites are more common than others (Cost and Boeke 1998; Feng et al. 1996; Jurka 1997).

Table 2.1 - PreTa L1 integration sites.

preTa L1 Integration Sites	Number
TTTT/A	60
TCTT/A	37
CTTT/A	20
TTTA/A	18
TTTC/A	18
TTTT/G	16
TTCT/A	14
TCTT/G	7
CTTT/G	5
ATTT/A	5
CTTT/C	5
TTTT/C	4
TGTT/A	3
TATT/A	3
TATT/G	3
TCTT/C	2
TTTC/C	2
TCTC/A	2
GTTT/A	2
ATTT/C	2
GCTT/T,TTTT/T,TTTG/A,TTTC/T,TTTC/T,TTGT/G, TTAT/A,TGAT/G,TCTT/T,TCAT/A,TATC/A,TATA/T, TAAA/C,GCTT/A,CCTT/A,CATT/G,CATT/A,ACTT/G, ACTT/A,ACTA/C,ACCT/A,ACAC/T,ACAA/A,AAAA/A	1 each

A large number of L1 preTa elements had no observable target duplication sites. One possible explanation for this observation is that these elements have relatively short target site duplications. Alternatively, these elements may represent forward gene conversion events of older pre-existing L1 elements that by mutation, have rendered their target site duplications unrecognizable. Some of these events may also represent integrations that have occurred independent of endonuclease cleavage, that has previously been proposed as a mechanism for the repair of doubled stranded breaks in DNA (Moore and Haber 1996; Morrish et al. 2002; Teng et al. 1996).

To further characterize the preTa L1 insertions, we determined the DNA base content for sequence blocks 1 and 2 kb flanking all preTa L1 insertion sites with target site duplications of at least 10 bp. Flanking sequence was then grouped according to GC content with only data for the 1 kb sequence blocks shown in figure 2.1. Our data suggests that preTa L1 elements integrate preferentially in genomic regions with GC content less than 36%, but are present in genomic regions with GC content as low as 26% and as high as 52%. A similar insertion site preference was observed for 2 kb sequence blocks as well as for the previously reported L1 Ta subfamily (Myers et. al 2002) and other L1 subfamilies (Szak et al. 2002). In addition, we also analyzed L1 preTa elements inserted in repetitive sequences and grouped them according to the repeat family in which they reside (Figure 2.2). This analysis showed that preTa L1 elements insert most frequently in other L1 elements, which is expected both because L1 sequences occupy a large percentage of the human genome and because L1 elements are less GC rich relative to other mobile element families, such as Alu elements, making them more susceptible to subsequent L1 integrations. Lastly, preTa L1 containing regions were analyzed to determine the distance from the integration to the nearest gene. Twelve L1 preTa elements reside within 25 kb of novel or

known genes as denoted by GenBank annotation, including one full length preTa element, L1AD242, which inserted into intron 23-24 of the retinoblastoma susceptibility protein 1 gene and accounts for 6072 bp of the 7988 bp intron.

Sequence Diversity

PreTa L1 sequence diversity is also created by variable 5′ truncation with some of the elements in the human genome only a few hundred base pairs in length, whereas some full-length elements are over 6000 base pairs. This phenomenon is classically attributed to the lack of processivity of the reverse transcriptase enzyme in the creation of the L1 cDNA. The point of truncation is traditionally believed to occur as a function of length, where shorter inserts are more likely to occur in the human genome than longer elements (Grimaldi et al. 1984). Our data show that there is an enrichment of full-length elements in the human genome, and like the Ta L1 elements many preTa L1 elements have been faithfully replicated in their entirety and inserted into new genomic locations. Of the 356 elements examined (362 total minus 6 elements located at the end of sequencing contigs), 97 were over 6000 base pairs long, representing a much larger L1 preTa size class than any other size class (Figure 2.3). By contrast, very few elements were found in the size ranges between 4000 and 5500 bases, with only 14 of the 356 elements truncated to this particular size range. A bimodal distribution in the size of the elements is created since there are a significant number of preTa L1 elements that are severely 5 prime truncated and those that are full-length with the average preTa element length of roughly 2700 bp and the median preTa element length of roughly 1600 bp. One hundred ninety-six elements were small with sizes less than 2000 bp, with 125 of these only 50-1000 bases in length. In addition 28% (100/356) of the preTa L1 elements examined were inverted at their 5 prime end, which is believed to occur by an event known as twin priming where target primed

reverse transcription is interrupted by a second internal priming event, resulting in an inversion of the 5 prime end of the newly integrated LINE element (Ostertag and Kazazian 2001). Although L1 truncation is most likely the result of the relatively low processivity of the L1 reverse transcriptase, processes that form secondary structures in the RNA or DNA strands present at the integration site, like twin priming, may also be associated with L1 truncation. One expectation of this model is that a common truncation point should exist for L1 preTa elements. However, from our data we were not able to identify any common truncation points. Similar to other L1 elements, preTa L1 elements exhibit a significant amount of sequence diversity in the 3 prime tails. In general, the 3 prime tails found in this L1 subfamily range in size from 4 to over 1600 bp in length. Sixty-four percent contain AT rich low complexity sequence, 13% have homopolymeric A tails with an average tail length of 15 bp, 6% have simple sequence repeats with the most common repeat family $TAAA_n$, and 17% contain complex sequence likely resulting from 3 prime transduction events. Three-prime transduction by L1 elements is a unique

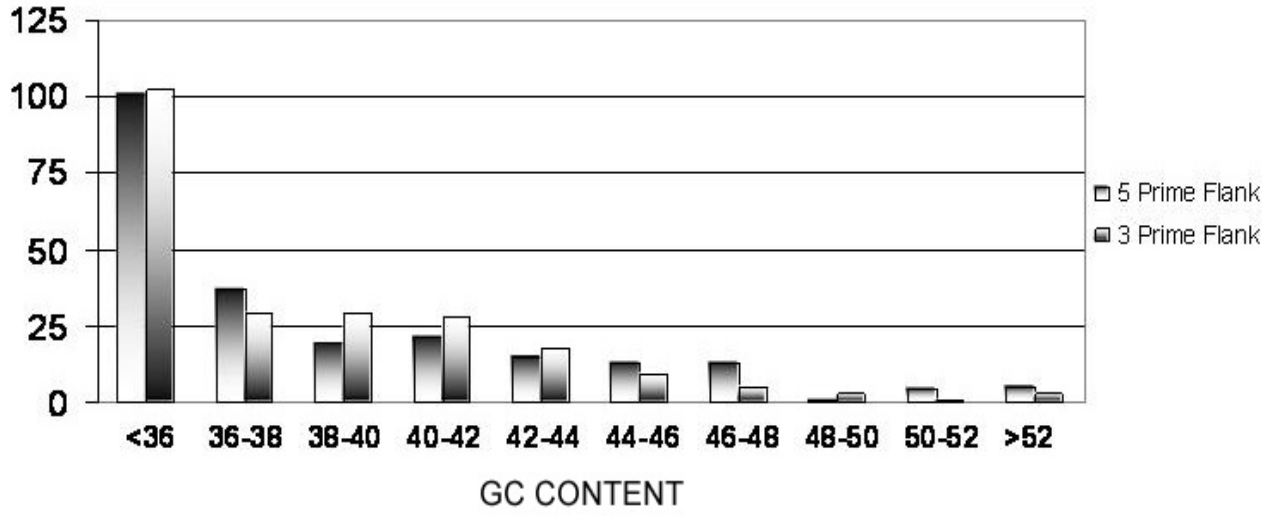

Figure 2.1

Figure 2.1 - Analysis of preTa L1 pre-integration sites. GC content was calculated for L1 insertion flanking sequences of 1 and 2 kb. The 1 kb results are shown here.

duplication event that occurs when an L1 sequence is transcribed along with genomic sequence at its 3 prime end. This sequence then integrates at a different genomic location resulting in duplication of the source L1 sequence and the 3 prime genomic sequence flanked by target site duplications (Boeke and Pickeral 1999; Goodier et al. 2000; Moran et al. 1999) . We have identified fifty 3 prime transduction events mediated by preTa L1 elements and believe that these elements have transduced approximately 10,400 total bases of sequence with one transduction event responsible for duplicating a region over 1600 bp. The diversity observed in the tails of the L1 elements is not surprising since previous studies have shown an association as well as direct evidence that simple sequence repeat motifs present in the 3 prime tail of mobile elements can mutate serving as nuclei for the generation of simple sequence repeats (Arcot et al. 1995; Economou et al. 1990; Ovchinnikov et al. 2001). A complete list of the preTa elements involved in transduction events is located at our web site (http://batzerlab.lsu.edu).

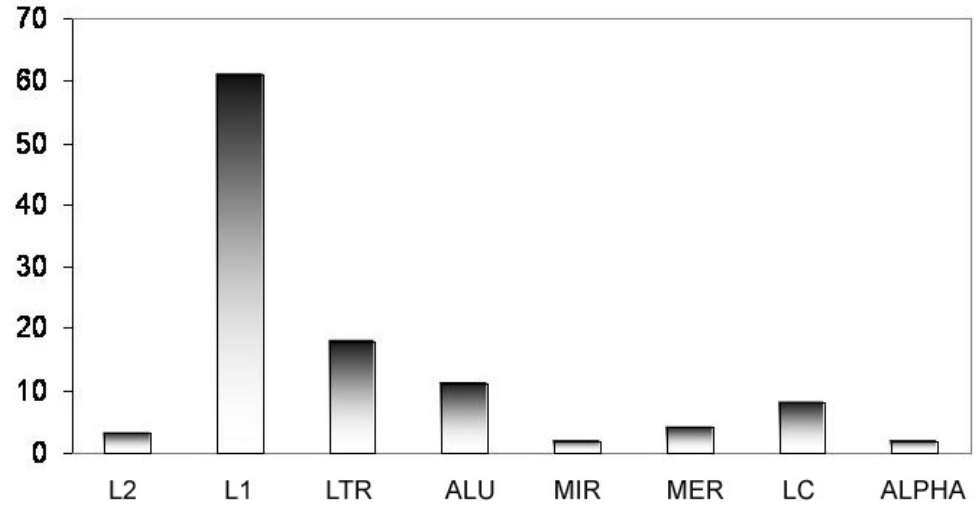

Figure 2.2

Figure 2.2 – PreTa L1 integrations within other repetitive elements. PreTa insertions within mobile elements were grouped according to the element in which they inserted. Mobile element categories include LINE-2 (L2), LINE-1 (L1), Long Terminal Repeats (LTR), Alu (ALU), Mammalian-wide Interspersed Repeats (MIR), Medium Reiteration Frequency Sequences (MER), Low Complexity Sequences (LC), Alphoid Satellite Repeats (ALPHA).

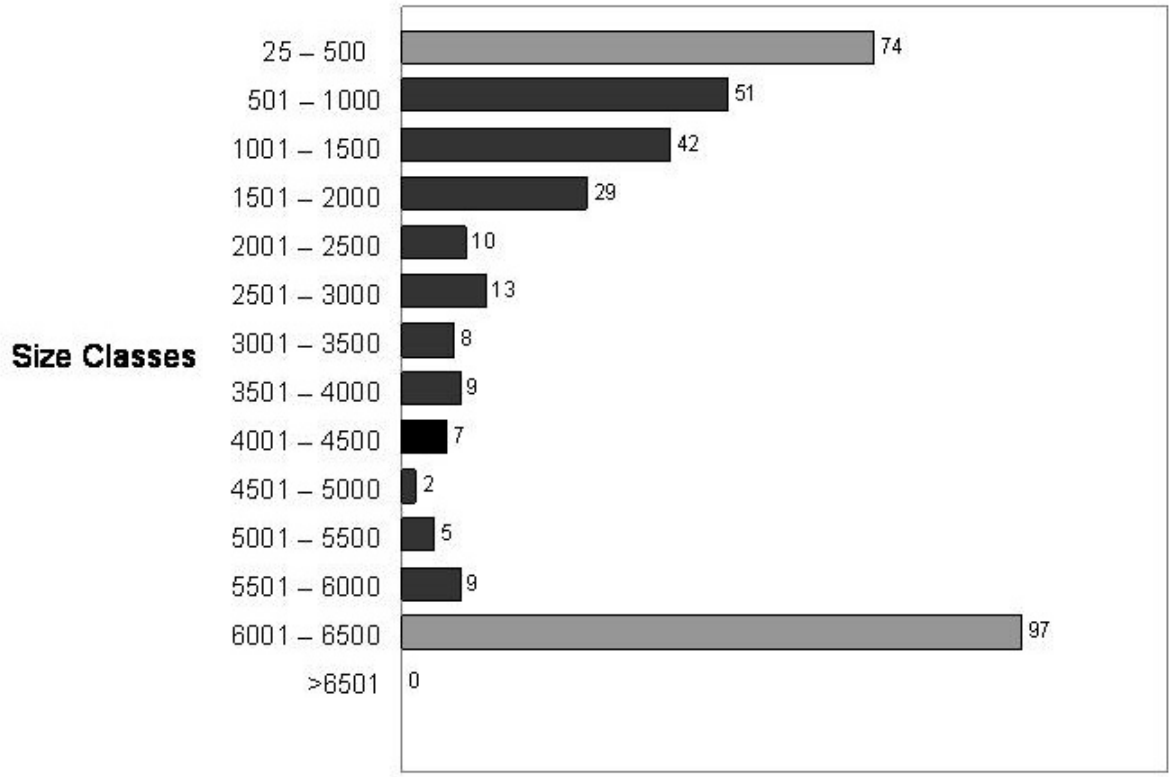

Figure 2.3

Figure 2.3 – PreTa element genomic size distribution. The following schematic shows the size distribution of preTa elements.Elements are grouped in 500 base pair intervals ranging from 25 bp in length to >6501 bp in length. The two most common size intervals are denoted in gray.

L1 Associated Human Genomic Diversity

Of the 362 L1HS preTa elements isolated *in silico*, 102 of the elements were inserted into other repetitive regions of the genome such that flanking unique sequence PCR primers could not be designed. Six additional elements resided at the end of sequencing contigs in GenBank and lacked unique flanking sequence information making PCR primer design in this region impossible. The remaining 254 were analyzed using a subfamily specific polymerase chain reaction assay and flanking unique sequence primers as previously described (Sheen et al. 2000) (summarized in Table 2.2). Three elements out of 254, produced inconclusive PCR results

because of the amplification of paralogous genomic sequences as described previously (Batzer et al. 1991). Nine elements produced non-specific PCR results, and were excluded from further analysis. Another nine elements produced subfamily-specific PCR products in all human samples tested, but did not produce pre-integration site in both human and non-human primate genomes. This may be the result of some type of large deletion event that occurred in the human genome and not in the genome of non-human primates making the non-human primate pre-integration site much larger than expected and not detectable by our assay as reported previously (Myers et al. 2002) . Alternatively this could also be the result of mutations in the oligonucleotide hybridization sites rendering them ineffective for PCR. In addition, we identified 36 preTa L1 elements that mapped to the X chromosome and eight that mapped to the Y chromosome, all of which were fixed present in the individuals tested (APPENDIX B Supplementary Data Table 1). The human genomic diversity associated with the autosomal preTa L1 elements is shown in Supplementary Data Table 1 and 2 (APPENDIX B).

Table 2.2 - Summary of preTa L1 analysis

LOCI ANALYZED BY PCR	254
Fixed present	200
High frequency insertion polymorphisms	11
Intermediate frequency insertion polymorphisms.	22
Low frequency insertion polymorphisms	0
Total preTa insertion polymorphisms	33
Inserted in paralogous sequences	3
No pre-integration site amplified in primates	9
No PCR results	9
LOCI ANALYZED NOT BY PCR	
L1 elements inserted in other repeats	102
End of contig	6
Total preTa L1 elements analyzed	362

Two hundred thirty three (254-9-9-3) preTa L1 elements produced unambiguous results when analyzed by a two-step PCR assay across 80 individuals from four geographically diverse human populations with 33 (14%) being polymorphic with respect to insertion presence/absence (APPENDIX B Supplementary Data Table 1 and 2). Examples of human genomic diversity associated with preTa L1 insertion polymorphisms are shown in Figure 2.4A and 2.4B. Eleven of the preTa L1 elements were high frequency insertion polymorphisms with L1 element allele frequencies greater than 0.70, so that most of the individuals were homozygous (+/+) for the presence of the LINE element. Twenty-two of the polymorphic elements were intermediate frequency, with a LINE element allele frequency greater than 0.30 but less than 0.70 across the diverse human populations sampled. None of the L1 preTa elements tested had insertion allele frequencies less than 0.30. One possible explanation for the absence of low frequency preTa insertion polymorphisms would be that the preTa subfamily has largely undergone retrotranspositional quiescence and is no longer generating new copies. As a result, the number of low frequency preTa insertion polymorphisms in the human genome would be limited. It is also possible that the newly integrated preTa L1 elements are removed from the human genome as a result of negative selection. However, we consider the former explanation more likely based upon the three-fold higher levels of insertion polymorphism in the Ta subfamily as compared to the preTa subfamily (45% vs. 15%) as well as the previously reported frequency distribution of Ta L1 insertion polymorphisms in the human genome (Myers et al. 2002) .

Two hundred L1 preTa L1 elements were fixed present. These elements are likely to be slightly older than their polymorphic counterparts, having inserted into the human genome prior to the radiation of humans from Africa. Overall, the unbiased heterozygosity values across all of the L1 elements subjected to PCR analysis were similar across the four populations with

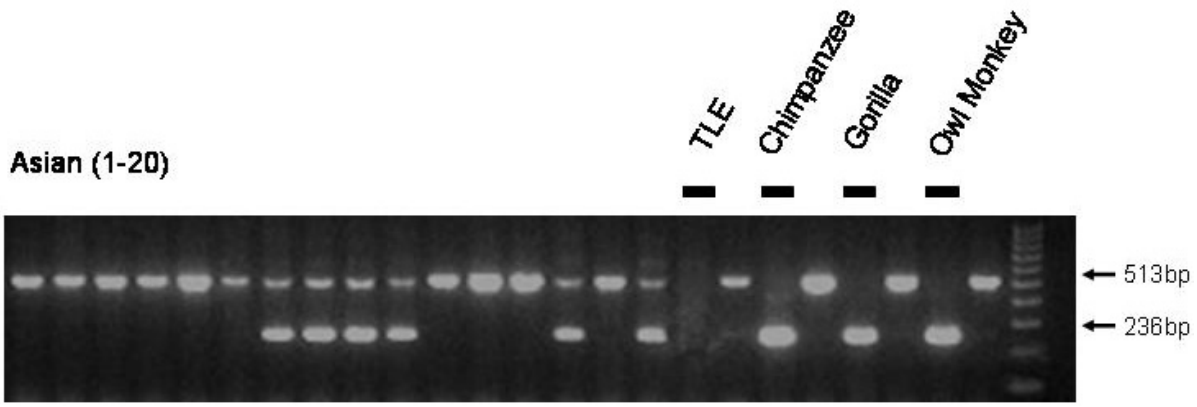

Figure 2.4A

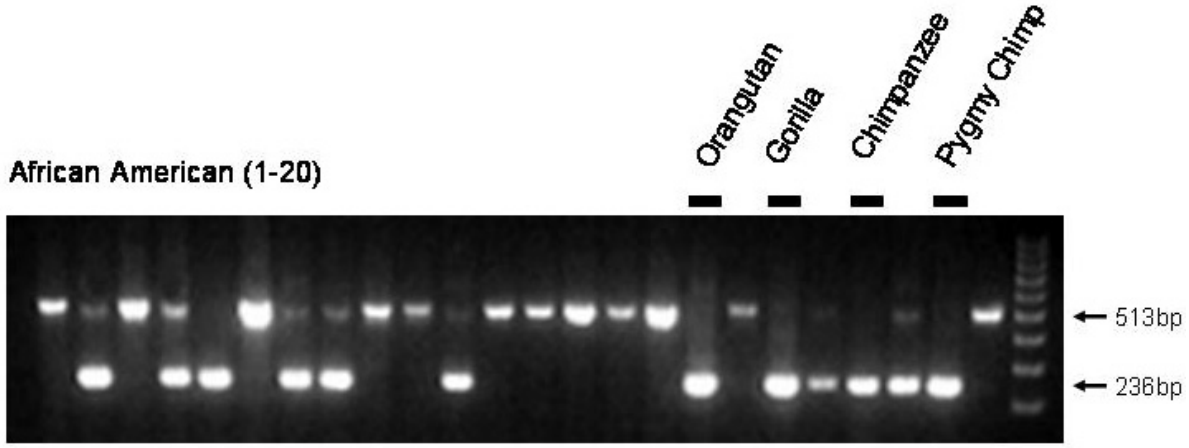

Figure 2.4B

Figure 2.4 PreTa L1 insertion polymorphisms. This figure is an agarose gel chromatograph of the PCR products from a survey of thfigure 2.4 1e human genomic variation associated with L1AD125. Amplification of the pre-integration site of this locus generates a 236 bp PCR product. Amplification of a filled site generates a 513 bp product (using flanking unique sequence primers). In this survey of human genomic variation 20 individuals from each of four diverse populations were assayed for the presence or absence of the L1 element, with Asian samples shown in figure 3A and African Americans shown in figure 3B. The control samples are denoted by the black lines and were TLE buffer (10 mM Tris-HCl: 0.1 mM EDTA), common chimpanzee, pygmy chimpanzee, gorilla, orangutan and owl monkey DNA templates. In addition, this particular L1 element was absent from the genomes of non-human primates.

values of 0.306 in African Americans, 0.243 in Asians, 0.252 in European Germans, and 0.269 in South Americans with the African American population being the most diverse with respect to preTa L1 alleles (APPENDIX B Supplementary Data Table 2).. However, several of the polymorphic elements individually exhibited unbiased heterozygosity values that approached 0.5, the theoretical maximum for bi-allelic loci.

In order to determine if the LINE insertion polymorphisms were in Hardy-Weinberg Equilibrium (HWE) we compared expected genotype frequencies with observed genotype frequency using chi-square tests for goodness of fit. A total of 132 chi-square tests for goodness of fit are theoretically possible. However, 28 of the comparisons involved populations that were monomorphic for the presence of the L1 insertion leaving 104 possible tests. A total of 23 deviations from Hardy-Weinberg expectations were observed in the comparisons. Eighteen of the deviations were the result of low expected genotype frequencies. Of the remaining five tests that deviated from HWE, none clustered by population or locus. This deviation is not surprising since a total of 5.15 deviations from HWE would be expected by chance alone at the 5% significance level. One short coming of this method is its inability to deal with low expected genotype frequencies. To further test these polymorphisms for HWE, we performed an exact test for Hardy-Weinberg proportions using the Markov chain test available in the Arlequin program (Guo and Thompson 1992) , which is not hindered by low expected frequencies. The test revealed that of the 104 comparisons none deviated from HWE proportions at the one percent level. Therefore we conclude that the newly identified L1 insertion polymorphisms do not significantly depart from HWE.

Discussion

Here we report a comprehensive analysis of the dispersion and insertion polymorphism associated with the preTa L1 subfamily within the human genome. We estimate that there are approximately 900 lineage specific L1 elements present in the entire human genome. In addition, given the median size for preTa and Ta L1 elements (~1600 bp) and a conservative copy number estimate of 900 elements, we estimate that human lineage-specific L1 retrotransposition has been responsible for increasing the size of the human genome by roughly 1.4 million bases.

The level of sequence diversity, estimated age, and the reduction of human genomic variation associated with this L1 subfamily relative to the L1 Ta subfamily provide strong evidence suggesting the expansion of preTa L1 elements began prior to the expansion of the L1 Ta subfamily that has been analyzed in detail previously (Boissinot et al. 2000; Myers et al. 2002). However, the expansion of preTa L1 elements also appears to have occurred over a time frame that predated the radiation of humans from Africa and continued until very recently, in fact it may still be occurring at a low level within the human lineage. Thus, we conclude that the expansion of preTa and Ta L1 elements occurred in an overlapping time frame in the human lineage. The reason(s) for the relative retrotranspositional quiescence of preTa elements remain unknown. However, they may relate to alterations in the ORF2 protein of the preTa elements, decreased transcription from the preTa "source" elements or a decrease in the ability of the elements to undergo target primed reverse transcription (Moran 1999). Further studies using *in vitro* systems to measure retrotransposition (Moran et al. 1996) will be required to definitively address this question.

Sequence analysis of the preTa L1 insertions suggest that they have a slight preference for integrating into regions of the genome with low GC content. This observation is contradictory to that previously reported (Ovchinnikov et al. 2001), but is in agreement with results obtained by The International Human Genome Sequencing Consortium (Lander et al. 2001). The reason for this integration site preference is unclear, but may result from a subtle sequence preference of the preTa encoded endonuclease. Alternatively, this observation may reflect limitations on L1 preTa insertion events imposed by chromatin organization. However, it is likely that both factors, as well as others not mentioned here, are important in determining where in the human genome young L1 elements will integrate. It is also interesting to note that some L1 preTa insertions have occurred adjacent to known genes. The persistence of these newly integrated preTa L1 elements in these regions of the human genome most likely is indicative that have had no negative effects with respect to the function of these genes.

Twenty-nine of the essentially 105 full length L1 preTa elements identified have both open reading frames intact and are presumably retrotransposition competent elements. The data collected from the L1 preTa subfamily along with the L1Hs Ta subfamily (44 elements) yields a computational estimate of 73 active L1 elements within the genome that is comparable to previous estimates of the number of potentially active L1 elements in the human genome (Sassaman et al. 1997). Collectively, these data suggest L1 elements from multiple subfamilies may still be capable of retrotransposition within the human lineage. In addition, it is also important to mention that those full-length elements that no longer have intact open reading frames could have previously served as active "source" or driver genes for the expansion of pre Ta L1 elements, but have accumulated mutations over time that subsequently inactivated them.

The computational identification approach described here provides an efficient and high-throughput method for recovering preTa L1 elements from the human genome, some of which are polymorphic for insertion presence/absence in individual human genomes. Individual L1 insertion polymorphisms identified, similar to other mobile element insertion polymorphisms, are the products of unique insertion events within the human genome. Because each L1 element integrates only once into the human genome, individuals that share L1 insertions (and insertion polymorphisms) inherited them from a common ancestor, making the L1 filled sites identical by descent (Myers et al. 2002; Sheen et al. 2000). This distinguishes L1 insertion polymorphisms from other types of genetic variation which may not be obtained from a single ancestral allele including microsatellites (Nakamura et al. 1987) and restriction fragment length polymorphisms (Botstein et al. 1980; Nakamura et al. 1987). In addition, the ancestral state of an L1 insertion is known to be the absence of the L1 element. Therefore the thirty-three new L1 insertion polymorphisms reported here appear to have genetic properties similar to the previously identified Alu (Batzer et al. 1991; Batzer et al. 1994; Hammer 1994; Jorde et al. 2000; Perna et al. 1992; Stoneking et al. 1997) and L1 (Boissinot et al. 2000; Myers et al. 2002; Sheen et al. 2000) insertion polymorphisms and provide a unique form of genetic variation present in the human population that will serve as an additional source of identical by descent genomic variability for the study of human population relationships.

Materials and Methods

Cell Lines and DNA Samples

The cell lines used to isolate primate DNA samples were as follows: human (*Homo sapiens*) HeLa (ATCC CCL2), common chimpanzee (*Pan troglodytes*) Wes (ATCC CRL1609), pygmy chimpanzee (*Pan paniscus*) Coriell Cell Repository Number AG05253, gorilla (*Gorilla*

gorilla) Lowland Gorilla (Coriell Cell Repository Number AG05251B), green monkey (*Cercopithecus aethiops*) ATCC CCL70, owl monkey (*Aotus trivirgatus*) OWK (OWKidney) ATCC CRL 1556, and Orangutan (*Pongo pygmaeus*) (Coriell Primate Panel PRP00001 Cell Repository Number NG12256) . Cell lines were maintained as directed by the source and DNA isolations were performed using Wizard genomic DNA purification (Promega). Human DNA samples from the German European, African American, and Asian population groups were isolated from peripheral blood lymphocytes (Ausabel et al. 1987) available from previous studies (Stoneking et al. 1997). South American Human DNA was obtained form Coriell Human Variation Panels HD17 and HD18.

Computational Analyses

The draft sequence of the human genome was screened using the Basic Local Alignment Search Tool (BLAST) (Altschul et al. 1990) available at the National Center of Biotechnology Information Genomic Blast page (http://www.ncbi.nlm.nih.gov/BLAST/). A 19 base pair oligonucleotide, 5'-CCTAATGCTAGATGACACG-3' that is diagnostic for the preTa subfamily was used to query the Human Genome database with the following the optional parameters: filter none; advanced options -e 0.1, -v 600, -b 600. Copy number estimates were determined from BLAST search results. Sequences containing exact matches were subjected to additional analysis as outlined below.

A sequence region of 9000-10000 bases, including the match and 1000-2000 bases of flanking unique sequence were annotated using RepeatMasker version 7/16/00 from the University of Washington Genome Center Server (http://repeatmasker.genome.washington.edu/cgi-bin/RepeatMasker) or Censor from the Genetic Information Research Institute (http://www.girinst.org/Censor_Server-Data_Entry_Forms.html)

(Jurka et al. 1996). These programs annotate repeat sequence content and were used to confirm the presence of preTa L1 elements and regions of unique sequence flanking the elements. PCR primers flanking each L1 element were designed using Primer3 software available at the Whitehead Institute for Biomedical Research (http://www-genome.wi.mit.edu/cgi-bin/primer/primer3_www.cgiand) and were complementary to the unique sequence regions flanking each L1 element. The resultant primers were screened with standard nucleotide-nucleotide BLAST [blastn] against the non-redundant (nr) and high-throughput (htgs) sequence databases to ensure they resided in unique DNA sequences. Primers residing in repetitive sequence regions were discarded and new primers designed if possible. A complete list of all the L1 elements identified using this approach is available from our website (http://batzerlab.lsu.edu). Individual L1 DNA sequences were aligned using MegAlign with the ClustalW algorithm and the default settings (DNAstar version 5.0 for Windows) followed by manual refinement.

PCR Amplification

PCR amplification of 255 individual L1 elements was carried out in 25 μl reactions containing 20-100 ng of DNA of template DNA, 40 pM of each oligonucleotide primer (Table 1), 200 μM dNTPs, in 50 mM KCl, 1.5 mM $MgCl_2$, 10 mM Tris-HCl (pH 8.4) and Taq DNA polymerase (1.25 Units). Each sample was subjected to the following amplification for 32 cycles: an initial denaturation of 150 seconds at 94 °C, one minute denaturation at 94 °C, one minute at the annealing temperature (specific for each locus), and an extension at 72 °C for one minute. Following the cycles a final extension was performed at 72 °C for ten minutes. For analysis, 20 μl of each sample was fractionated on a 2% agarose gel with 0.05 μg/ml ethidium bromide. PCR products were directly visualized using UV fluorescence. The human genomic

diversity associated with each L1 preTa element was determined by the amplification of 20 individuals from each of four geographically distinct populations (African American, Asian, European, and South American) for a total of 160 chromosomes.

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CHAPTER THREE:

ANALYSIS OF THE HUMAN *ALU* Ya-LINEAGE*

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Introduction

SINEs (Short INterspersed Elements) are retroposable genetic elements typically less than 500 nucleotides long that are interspersed ubiquitously throughout different genomes (Deininger and Batzer 1993; Shedlock and Okada 2000). *Alu* elements are the most successful primate SINEs and have amplified to more than one million copies in primate genomes (Batzer and Deininger 2002). *Alu* elements mobilize by a mechanism termed target-primed reverse transcription, in which an *Alu* RNA transcript is reverse-transcribed into a DNA molecule that subsequently reintegrates into a new genomic site (Boeke 1997; Feng et al. 1996; Kajikawa and Okada 2002; Luan et al. 1993; Mathias et al. 1991; Sinnett et al. 1992). As *Alu* elements do not produce any of the proteins needed to facilitate their movement or retroposition, they must instead capitalize on the ORF2 product of Long INterspersed Elements (LINEs) that encodes the endonuclease and reverse transcriptase activities needed for mobilization (Dewannieux et al. 2003; Feng et al. 1996; Kajikawa and Okada 2002; Mathias et al. 1991). This method of "borrowing" LINE mobilization factors has enabled *Alu* elements to reach high copy numbers in both human and non-human primate genomes.

Although there are many copies of *Alu* elements in the human genome, only a few are believed to be retropositionally competent (Batzer et al. 1990; Deininger et al. 1992; Leeflang et al. 1993; Leeflang et al. 1992). The accumulation of new mutations within these active 'master' or 'source' genes, results in the creation, through evolutionary time, of new *Alu* subfamilies or lineages of elements with common diagnostic mutations (Carter et al. 2004; Deininger et al. 1992). Specific *Alu* subfamilies can be identified by their diagnostic mutations (Shen et al. 1991; Slagel et al. 1987; Willard et al. 1987). Some "young" *Alu* subfamilies have amplified so recently in humans that they are largely absent from the genomes of non-human primates, or are

lineage specific inserts within different primate taxa (Batzer and Deininger 2002; Roy et al. 1999). These evolutionarily recent *Alu* insertions are useful for the study of human population genetics and non-human primate phylogenetics (Batzer et al. 1996; Batzer et al. 1994; Jurka and Pethiyagoda 1995; Roy-Engel et al. 2002; Roy-Engel et al. 2001; Salem et al. 2003; Sherry et al. 1997; Stoneking et al. 1997).

"Young" subfamilies typically have a large number of human-specific insertions, share a higher number of diagnostic point mutations and contain some loci, which are still polymorphic with respect to their presence or absence in diverse human populations. The *Alu* Ya-lineage is the largest "young" evolutionarily-related group of *Alu* elements in the human genome. The Ya-lineage is comprised of Ya5 elements, that have all five diagnostic mutations as well as smaller subfamilies, which contain less than five of the diagnostic mutations. Subfamilies that contain other mutations in addition to having all five diagnostic mutations, such as Ya8 and Ya5a2, are also considered a part of the Ya-lineage and have been characterized previously (Roy et al. 1999; Roy et al. 2000). Here, we survey 2318 autosomal Ya-lineage *Alu* elements containing five or fewer diagnostic mutations from the human genome draft sequence and the human genomic diversity associated with these elements.

Results

Ya-lineage Element Copy Number and Chromosomal Distribution

A total of 2482 Ya-lineage elements possessing one to five diagnostic mutations were recovered from the human genome draft sequence. The autosomes and sex chromosomes contain a total of 2318 and 164 elements, respectively (Callinan et al. 2003). A total of 615 autosomal elements integrated within other repeated sequences and were therefore not amenable to further polymerase chain reaction (PCR)-based analyses. Another 232 produced inconclusive PCR

results and one element was located at the end of a sequencing contig (*e.g.* not enough flanking 3' genomic sequence to develop an oligonucleotide primer). Of the 1470 autosomal elements that could be analyzed by PCR, 18 were inserted in paralogous sequences, 1139 were present on both chromosomes of all individuals tested (fixed present) and 313 were polymorphic for insertion presence/absence in diverse human populations (Table 3.1).

Table 3.1 - *Alu* Ya-lineage element PCR analysis summary[1,2]

	***Alu* Ya-lineage elements**
Loci analyzed by PCR	**1470**
Fixed present	**1139**
High frequency insertion polymorphisms	**15**
Intermediate frequency insertion polymorphisms	**264**
Low frequency insertion polymorphisms	**34**
Total polymorphic	**313**
Paralog	**18**
Loci not analyzed by PCR	**848**
Inserted in other repeats	**615**
No PCR results	**232**
End of contig	**1**
Total autosomal elements analyzed	**2318**
Total sex chromosome elements analyzed*	**164**

[1] Sex chromosome data previously analysed by Callinan et al. 2003.
[2] A full summary of GenBank accession numbers, PCR primers and conditions, and PCR amplicon sizes for these loci are shown in APPENDIX B Supplementary Data Table 3.

A χ^2 "goodness of fit" test was performed on the chromosomal distribution data to test a model of random insertion for the *Alu* Ya-lineage elements in which the number of expected insertions on each chromosome is proportional to the percentage of the genome that each chromosome represents (Table 3.2). The genome-wide, chromosomal distribution was assessed based on a total number of elements recovered from the human genome draft sequence. Human chromosomes 15, 18, 21 and 22 were statistically different from the random insertion model at

the 5% significance level with expected numbers greater than the observed number of elements. Chromosomes 1, 6, 7, 12, 13, 14, and 19 were statistically different at the 5% significance level with observed numbers greater than what would be expected based upon a random insertion model.

Table 3.2 - Chromosomal distribution of autosomal *Alu* elements

Chromosome	% of human genome	# observed of *Alu* elements	# of expected *Alu* elements	S/NS[1]
1	8.01%	213	184	S
2	7.93%	206	182	NS
3	6.54%	166	150	NS
4	6.28%	151	144	NS
5	5.96%	146	137	NS
6	5.59%	152	129	S
7	5.16%	154	119	S
8	4.80%	99	110	NS
9	4.36%	95	100	NS
10	4.41%	91	101	NS
11	4.48%	118	103	NS
12	4.37%	125	101	S
13	3.65%	114	84	S
14	3.32%	104	76	S
15	3.17%	48	73	S
16	2.99%	62	69	NS
17	2.76%	62	64	NS
18	2.56%	43	59	S
19	1.95%	60	45	S
20	2.06%	52	47	NS
21	1.47%	20	34	S
22	1.57%	18	36	S
X	4.97%	119	114	NS
Y	1.65%	45	38	NS
Total # elements[2]		**2299**		

[1] Statistically significant (S) or not statically significant (NS) at 5% level.
[2] Total # of elements = fixed present + polymorphic + *Alu* elements with failed PCR results + *Alu* elements within other human repeats

Ya-lineage Sequence Attributes

The length of direct repeats flanking individual Ya-lineage *Alu* elements range from 4-23 base pairs in length with an average length of 13 base pairs. Exactly 120 elements contain no detectable direct repeat sequences. *Alu* Ya-lineage element oligo-(dA)-rich tails ranged from 3 to

115 base pairs in length with an average of 27 base pairs. Approximately 4.4% (102/2315) of the elements contain tails with simple sequence repeats (≥ 4 consecutive units). Only three Ya elements did not have detectable oligo-(dA)-rich tails.

Recombination, incomplete reverse transcription or improper integration into the genome could cause sequence truncations in individual *Alu* elements according to the contemporary model of *Alu* genomic movement and integration (Feng et al. 1996; Luan et al. 1993; Moran et al. 1996). There are 95% more truncations in the 5' region of the Ya-lineage elements compared with the 3' region, which is consistent with the current *Alu* retrotransposition model, since it posits that reverse transcription initiates at the 3' end of the source or "master" *Alu* sequence (Jurka and Klonowski 1996). A total of 280 autosomal Ya-lineage *Alu* elements were found to have collectively lost 9172 base pairs of 5' *Alu* sequence. Investigation of the 3' ends showed that 583 base pairs are missing from 15 autosomal elements.

Flanking Genomic Sequence Content

Ya-lineage elements that have integrated directly adjacent to other human repeats and are not amenable to PCR, were analyzed for human repeat content. Of these elements, 47% (289/615) integrated within or next to LINE-1 elements, 22% (135/615) integrated next to evolutionarily older *Alu* elements and the remaining 31% (191/615) integrated next to LTR (Long Terminal Repeats), MER (MEdium Reiteration frequency sequences), LC (Low-Complexity sequences) and SSRs (Simple Sequence Repeats). A total of twenty-eight autosomal Ya-lineage elements contain an independent, full-length *Alu* element either in the oligo(dA)-rich tail or immediately adjacent to it, such that both elements are contained within a single set of direct repeats; data are available on our webpage (http://batzerlab.lsu.edu). One thousand bases of 5' and 3' genomic sequence flanking each *Alu* element were analyzed for GC content. The

mean GC content for the 5' and 3' flanking sequence was 39.1 and 39.2, respectively. The total mean GC content (including *Alu* element) is 41.0% in these genomic regions.

Paralogous Insertions

Paralogous insertions are *Alu* elements that have inserted into duplicate genomic loci and consequently, contain identical or nearly identical flanking genomic sequence. Computational searches for paralogous elements were performed using direct repeats and flanking oligonucleotide primer sequences as search criteria. However, this approach did not yield all existing paralogous *Alu* elements, with some additional elements recovered during the PCR stage. Our analysis yielded a total of 18 autosomal paralogs (Table 3.1). Analysis of a monochromosomal hybrid cell line DNA panel was used to determine the chromosomal location of the duplicated *Alu* elements (see Materials & Methods). Eleven *Alu* elements were found in regions that duplicated on the same chromosome. Six are in regions that duplicated onto two different chromosomes and one element is in a genomic region that duplicated onto three different chromosomes.

Insertion Polymorphisms

Four major continental populations (African American, Asian, European and South American) were analyzed to determine the *Alu* Ya-lineage-associated human genomic diversity. A total of 313 polymorphic *Alu* elements were identified on the human autosomes and nine have been previously reported on the X chromosome (Table 3.1) (Callinan et al. 2003). It is very likely that more than 313 polymorphic Ya-lineage elements exist in the human genome, since the draft sequence of the human genome is a composite derived from only a few individuals. PCR amplification of human autosomal Ya loci revealed an overall polymorphism rate of 22% (313/1452). A total of 78% (244 elements) of the polymorphic Ya-lineage loci had all five of the

subfamily specific diagnostic base mutations. Average heterozygosity and allele frequency data for the autosomal polymorphic loci were calculated (APPENDIX B Supplementary Data Table 4). Individual autosomal chromosome insertion polymorphism rates ranged from 11% (chromosome 9) to 40% (chromosome 21). A table of genome-wide human insertion polymorphisms is available on our website (http://batzerlab.lsu.edu).

Alu elements were categorized as either polymorphic or fixed present (FP). Fixed present is defined as when every individual tested has the *Alu* element on both chromosomes. Polymorphic elements were further classified as high (HF), intermediate (IF) or low frequency (LF). The following frequency classifications have been previously established (Carroll et al. 2001). Low frequency insertion polymorphisms are those exhibiting insertion frequencies of less than 30%. Intermediate frequency insertion polymorphisms are those loci where the *Alu* element is present at frequencies ranging from 30 to 70%. High frequency insertion polymorphisms are characterized by greater than 70% insertion frequency. High, intermediate and low frequency categories comprise 4.70% (15), 84.3% (264) and 11.0% (34) of the total autosomal *Alu* polymorphisms, respectively. Autosomal and X-chromosome positions of all Ya-lineage polymorphic elements were determined using BLAT screening (The BLAST-Like Alignment Tool) (http://genome.ucsc.edu/cgi-bin/hgBlat?hgsid=5329687) and Ensembl Human Genome Server (http://www.ensembl.org/) (Figure 3.1A and 3.1B) (Kent 2002; M. Clamp 2003).
A total of 901 χ^2 "goodness of fit" tests were performed. These yielded a total of 42 deviations from Hardy-Weinberg Equilibrium (HWE) ($p < 0.05$). Approximately 45 deviations would be expected by chance alone at the 5% significance level. A total of 16 of the 42 deviations were the result of poor-quality PCR amplification. Due to the fact that a large number of statistical tests were performed and none of the significant departures cluster by locus or population, we believe

Figure 3.1. Chromosomal distribution of polymorphic Ya elements. The physical location of each *Alu* Ya-lineage insertion polymorphism is shown. The polymorphic *Alu* elements were classified as: high (H), intermediate (I) or low (L) frequency insertion polymorphisms, as outlined in the text. Physical chromosomal location of each Ya-lineage *Alu* element was identified with BLAT and Ensembl Genome Web Browser. Elements represented here are classified according to allele frequency as: high frequency (HF), intermediate frequency (IF), low frequency (LF) or as fixed present (FP) insertions. Fixed Present: every individual tested had the *Alu* element in both chromosomes. Low frequency insertion polymorphism: the element is present in no more than 1/3 (33%) of alleles tested. Intermediate frequency insertion polymorphism: the element in present in more than 1/3 (33%) of alleles tested and no more than 2/3 (67%) of the alleles. High frequency insertion polymorphism: the element is present in no more than 2/3 (67%) of all alleles tested.The Ya-lineage *Alu* elements located on the sex chromosomes have been reported previously (Callinan et al. 2003).

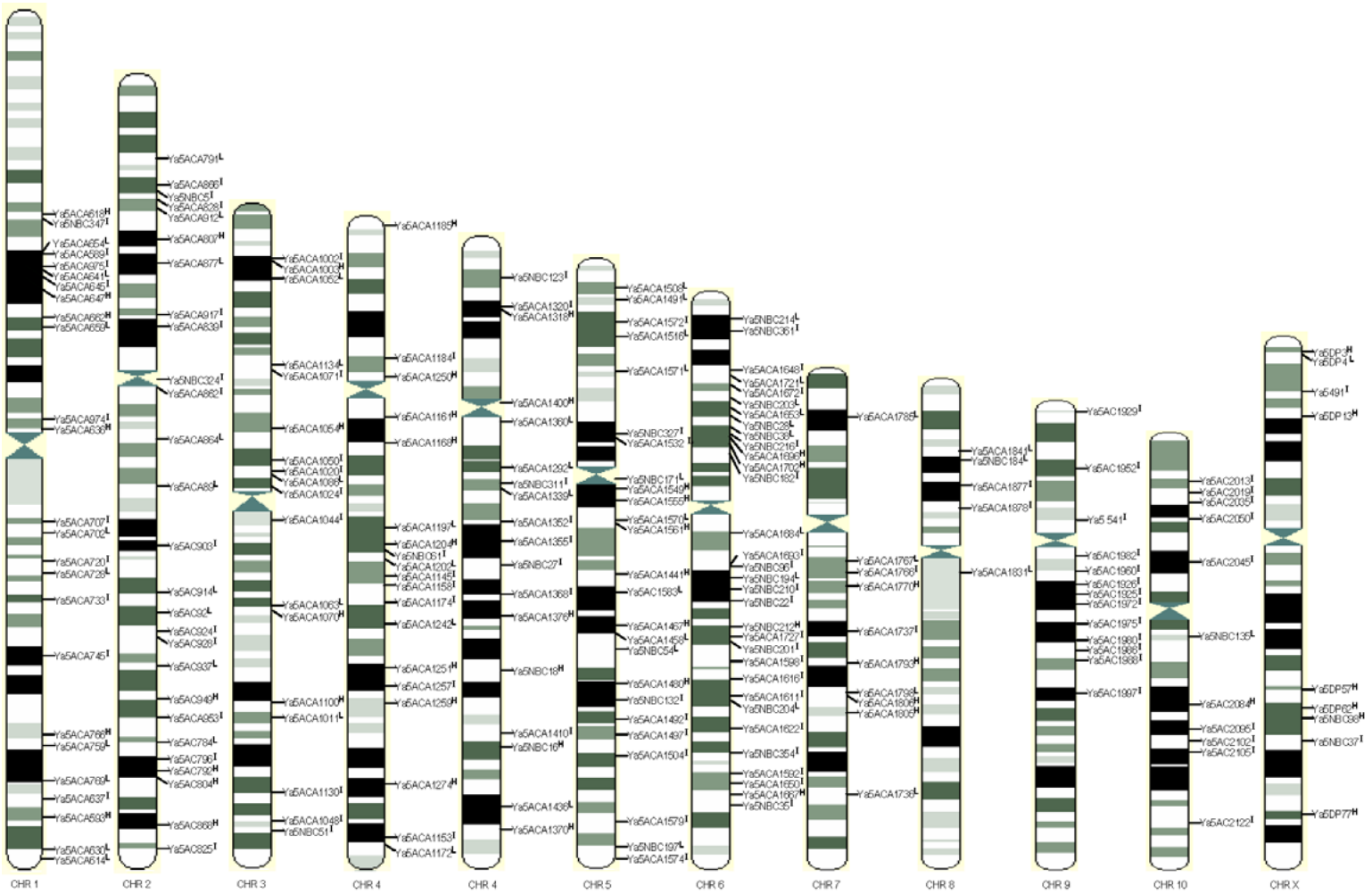

Figure 3.1A

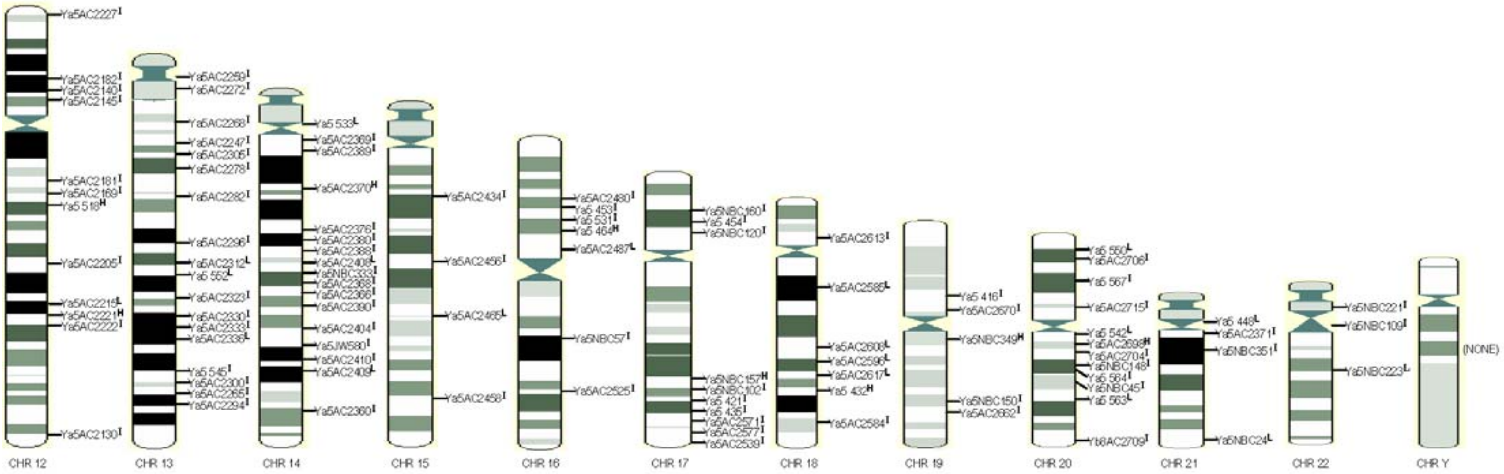
CHR 12
CHR 13
CHR 14
CHR 15
CHR 16
CHR 17
CHR 18
CHR 19
CHR 20
CHR 21
CHR 22
CHR Y
(NONE)

Figure 3.1B

the remaining 26 deviations represent normal statistical fluctuation and conclude that the Ya-lineage *Alu* insertion polymorphisms do not deviate from HWE. In addition, a Markov-Chain based analysis was applied to the data using the software Arlequin (Carlo 1992; Schneider 2000). Out of 901 comparisons, the test suggested that only 17 were significant, which is lower than what would be expected by chance alone at the 5% significance level. Thus, the results of both tests suggest that Ya-lineage *Alu* insertion polymorphisms as a whole do not significantly depart from HWE.

Analysis of Polymorphic *Alu* Insertion Loci

Overall heterozygosity values for polymorphic *Alu* insertion loci in African American, Asian, European and South American populations were calculated as 0.35, 0.32, 0 .34 and 0.33, respectively. Pairwise χ^2 tests of independence were performed between population-specific genotype distributions for each of the loci. The percentage of pairwise tests that showed a significant difference (at the 5% significance level) were as follows: African American vs. Asian (45%); African American vs. European (39%); African American vs. South American (32%); Asian vs. European (31%); Asian vs. South Americans (23%) and European vs. South American (15%). We examined the distributions of all the polymorphic loci further to identify loci that showed variability in only one population. Sixteen loci were polymorphic only in the African American population and monomorphic (present) in all others. Eleven loci were polymorphic only in African American population while being monomorphic absent for all others. The European population contained five such loci, two of which were monomorphic present for the other populations and three of which were monomorphic absent from other populations. The South American population contained two *Alu* loci that were polymorphic in that population with one being monomorphic fixed for the additional populations and one being

monomorphic absent for the other populations. The Asian population contained no examples of population specific allele variability. Lastly, we calculated the total polymorphism rate for each major population. The level of polymorphism in African Americans was 19%, Asians were 13%, Europeans were 15% and South Americans were 13%.

Evolutionary Age Estimates

The *Alu* Ya-lineage is made up of several groups or subfamilies with varying number of diagnostic mutations (Carroll et al. 2001). In this paper, we refer to these constituent groups as *subfamily-Ya1, -Ya2, -Ya3, -Ya4, -Ya5, -Ya5a2* and *-Ya8* in which each is named according to the number of diagnostic mutations contained within the consensus sequence (Batzer et al. 1996). Evolutionary age estimates of s*ubfamlilies-Ya5a2* and *-Ya8* have been reported previously (Roy et al. 1999; Roy et al. 2000). The *Ya5* subfamily is the largest group comprising greater than 75% of the entire Ya-lineage. CpG dinucleotide and non-CpG nucleotide mutation densities and neutral mutation rates of 0.90%/million years for CpG bases and 0.15%/million years for non-CpG bases were used to calculate the average evolutionary age of the Ya5 subfamily as reported (Batzer et al. 1990; Carroll et al. 2001; Labuda and Striker 1989; Miyamoto et al. 1987). The autosomal Ya5 elements were used in both CpG and non-CpG mutation calculations to determine age estimates. The CpG based age estimates yielded an average age of 2.27 my (million years). Non-CpG age estimates yielded an average age estimate of 2.56 my for the Ya5 *Alu* elements.

***Alu* Ya-lineage Origin and Orthologous Insertions**

Non-human primate DNA was subjected to PCR analysis with the same primers designed to detect individual human *Alu* insertion loci. This resulted in the recovery of five non-human primate loci that appeared to contain Ya-lineage *Alu* elements. DNA sequence analysis of these

loci however, showed that these orthologous loci contain older pre-existing *Alu* elements from other subfamilies or other non-repetitive genomic sequences (Table 3.3). Only one genuine Ya5 is known to exist in an orthologous locus which resides in a number of primate lineages (Leeflang et al. 1993; Leeflang et al. 1992). To date, eight Ya-lineage loci have yielded PCR results indicative of the presence of an *Alu*-filled site at orthologous positions in non-human primate genomes. All eight human loci contain Ya5 subfamily members. Three of these elements (Ya5NBC42, Ya5NBC91 and Ya5NBC188) have previously been sequenced in non-human

Table 3.3 - *Alu* Ya inserts in non-human primate orthologous loci[1]

Alu element	Human	Common chimpanzee	Pygmy chimpanzee	Gorilla	Orangutan	Green monkey	Spider monkey	Type
Ya5ACA1808	+(Ya5)	+(*Alu* Y) Plus 318 base pairs of genomic sequence	+(*Alu* Y) Plus 318 base pairs of genomic sequence	+(*Alu* Y) Plus 318 base pairs of genomic sequence	0	0	0	GC & Del
Ya5ACA1267	+(Ya5)	-	-	-	-	0	ERV of 629 base pairs	Ind
Ya5ACA1786	+(Ya5)	+(*Alu* Sq)	+(*Alu* Sq)	0	0	0	0	GC
Ya5ACA1792	+(Ya5)	-	-	-	-	-	+(*Alu* Sc)	Ind
Ya5ACA2578	+(Ya5)	Non-repetitive sequence	Non-repetitive sequence	Non-repetitive sequence	Non-repetitive sequence	0	0	Del

[1] +, Polymerase chain reaction (PCR) product indicates presence of *Alu* insert; –, small PCR product indicates absence of an *Alu* insert; 0, no PCR product of the locus was observed; GC, gene conversion; Ind, independent insertion; Del, *Alu*-mediated deletion

primates and have been shown to contain evolutionarily older *Alu* elements. The authors report that the results seen can be explained by the two evolutionary mechanisms, gene conversion or parallel independent insertions (Roy-Engel et al. 2002). The remaining five (Ya5ACA1808, Ya5ACA1267, Ya5ACA1786, Ya5ACA1792 and Ya5AC2578) are newly reported Ya-lineage elements that yield a filled site amplicon in at least one non-human primate genome. DNA sequence analysis of these non-human primate loci determined that these *Alu* insertions were not

authentic Ya-lineage insertions but rather *Alu* Y, Sc or Sq elements. Comparisons between human and non-human primate DNA sequences showed that three evolutionary mechanisms generated these results: gene conversion, *Alu*-mediated deletion or independent parallel insertion (Table 3.3). These forms of non-traditional *Alu* sequence evolution have been reported previously (Arcot et al. 1998; Batzer et al. 1995; Cantrell et al. 2001; Kass et al. 1995; Kass et al. 2000; Maeda et al. 1988; Nikaido 1999; Roy et al. 2000). Elements Ya5ACA1267 and Ya5ACA1792 demonstrate insertions at human and spider monkey loci but no insertion at additional nonhuman primate loci. The most parsimonious explanation in these cases would be two independent insertion events, as competing explanations would require either multiple deletion events among several primate lineages or both deletion and insertion events occurring on the lineage leading to humans. For locus Ya5ACA1267 this is further evidenced by the fact that the two insertions occurred at slightly different locations. The case is less clear for Ya5ACA1792, as subsequent sequence rearrangements/deletions in the spider monkey lineage have obscured the insertion point. Locus Ya5AC1808 appears to have resulted when a young Ya5 element inserted near a pre-existing Y element. A nonhomologous recombination between the two elements then occurred, which resulted in the partial conversion of the *Alu*Y element into an *Alu*Ya5 and deletion of approximately 300bp intervening sequence. Alignments of human and non-human primate orthologous sequences of the five newly reported unusual loci can be found on our website (http://batzerlab.lsu.edu). Locus Ya5ACA1786 appears to be an authentic gene conversion, with a older Sq element sequence being converted to an *Alu* Ya5 element.

Discussion

Here we report 2318 unique autosomal *Alu* Ya-lineage loci resulting in a total of 2482 Ya-lineage members possessing five or fewer diagnostic mutations that have been recovered

from the draft sequence of the human genome. The number of these Ya-lineage *Alu* elements recovered from the draft sequence compares favorably to previously published estimates of the size of this *Alu* subfamily (Batzer et al. 1995; Batzer et al. 1994; Carroll et al. 2001; Roy et al. 2000). A total of 1625 elements have been analyzed via PCR-based assays on the autosomes and sex chromosomes (Callinan et al. 2003; Carroll et al. 2001). With a polymorphism rate of 22% for the *Alu* Ya-lineage, 510 polymorphic *Alu* repeats would be expected from the 2318 autosomal elements analyzed. We would expect 323 elements from the loci analyzed by PCR (1470 elements) to be polymorphic. A total of 313 Ya-lineage autosomal *Alu* insertion polymorphisms have been recovered in this study (Table 3.1). The present study only recovered those polymorphic elements that have inserted alleles present in the genomes of the few individuals whose DNA constitutes the human genome draft sequence. As a consequence, approximately 50% of the actual loci that exist in human populations will be missed (Hedges et al. 2004). In addition, a number of polymorphisms may have been missed as a result of our inability to examine them using PCR assays because they either inserted in paralogous loci, inserted next to or within other human repetitive elements or simply landed in a genomic region that was not amplifiable by PCR.

Separate Ya-lineage subfamilies emerge as a result of an accumulation of diagnostic mutations occurring within ‘source’ or ‘master’ *Alu* genes over the course of primate evolution. The result is a series of evolutionary subfamilies which make up the entire Ya-lineage. The number of subfamily members differs between the different *Alu* subfamilies. The Ya5 subfamily is comprised of those elements that have five diagnostic mutations. The Ya5 average age calculated using non-CpG and CpG mutations was estimated to be 2.56my and 2.27my, respectively. The Ya5 *Alu* subfamily constitutes approximately 75% (1857 elements) of the

entire Ya-lineage. The second largest "young" *Alu* lineage, the Yb, is similar in subfamily structure to the Ya-lineage (Figure. 3.2A and 3.2B) (Carter et al. 2004). The Yb8 subfamily has an evolutionary age of approximately 2.39my and makes up 57% (1055/1851) of the entire Yb-lineage. Assuming the Ya5 subfamily had a linear rate of amplification, the age of the oldest individual member can be calculated as twice the average calculated evolutionary age. Both age estimates show that the oldest Ya5 elements integrated into the primate lineage approximately 5.12 (2.56 × 2 for non-CpG) and 4.54 (2.27 × 2 for CpG) million years ago assuming a linear amplification rate. This time corresponds to the time of the human and African ape divergence of four to six million years ago (Batzer and Deininger 1991; Roy et al. 1999; Roy-Engel et al. 2001). Thus, we expect to potentially see some Ya5 *Alu* elements in non-human primate genomes.

Previous studies have shown that Ya-lineage elements exists in gorilla, chimpanzee and orangutan genomes (Leeflang et al. 1993; Leeflang et al. 1993; Leeflang et al. 1992; Shaikh and Deininger 1996; Shen et al. 1991). Two have been found in gorilla in which one is unique to the gorilla genome and the other is believed to be a progenitor or "founder" locus (previously identified as EPL locus) of Ya5 *Alu* elements (Leeflang et al. 1993; Shaikh and Deininger 1996). This element contains all five diagnostic mutations and resides in chimpanzee and human orthologous positions making it the only known Ya-lineage locus shared among the three species (Matera et al. 1990). The founder (EPL) locus has also been traced to the orangutan (Leeflang et al. 1993; Shaikh and Deininger 1996). The founder locus is designated as Ya5ACA1363 in this study and is located on chromosome 5. There are a number of Ya5 elements that are unique to the chimpanzee genome and have been researched previously (Leeflang et al. 1993; Leeflang et al. 1992; Schmid 1996; Schmid 1998). These data, taken with the evolutionary age estimates

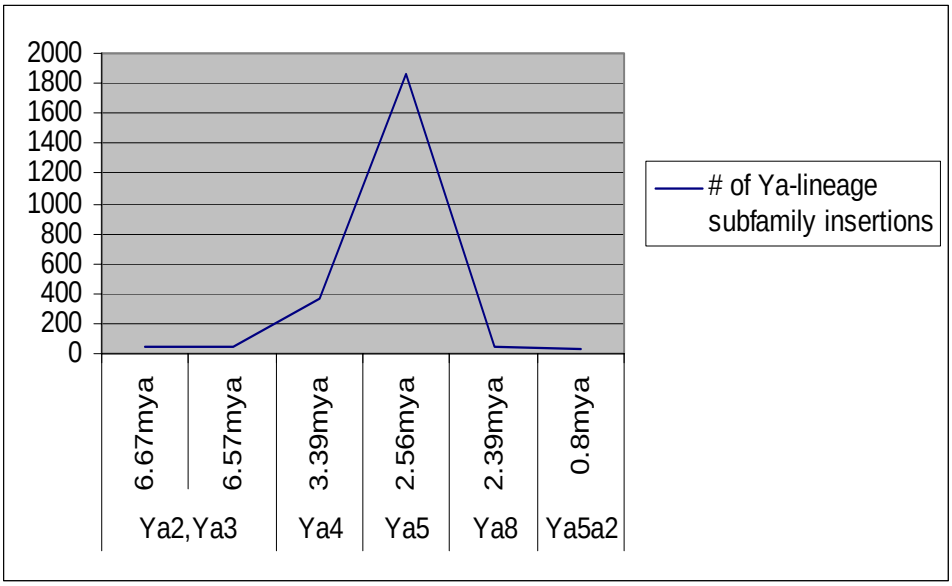

Figure 3.2A

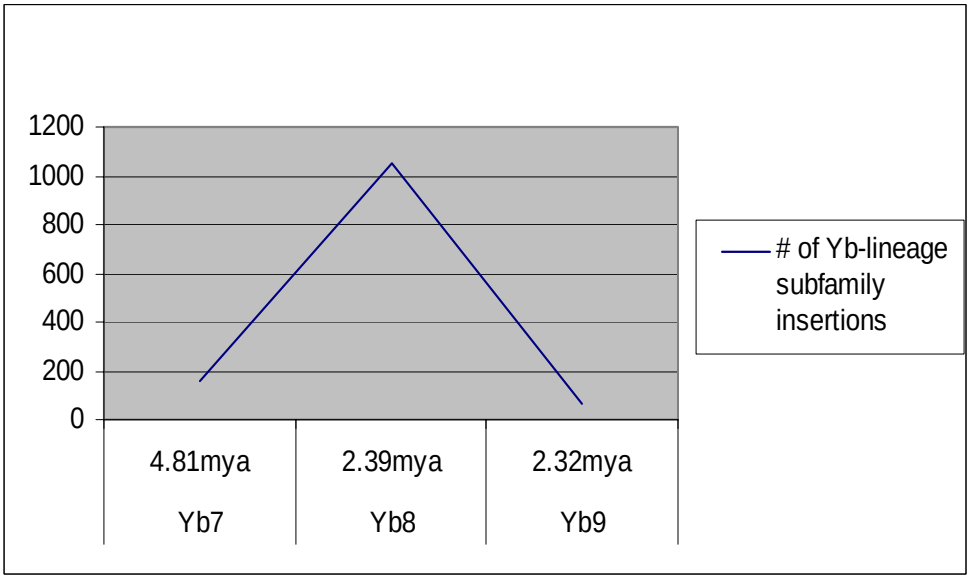

Figure 3.2B

Figure 3.2. *Alu* subfamily copy numbers and expansion times. A) The *Alu* Ya-lineage expansion throughout evolutionary time. *Subfamily-Ya5* constitutes approximately 75% of the entire lineage and has an average evolutionary age of 2.56my. Additional subfamilies with greater than five diagnostic mutations are part of the Ya-lineage but were not examined in this study.(Roy et al. 1999; Roy et al. 2000) Notation: my = million years. **B)** The Yb-lineage subfamily amplification throughout evolutionary time. Yb8 subfamily constitutes approximately 57% of the entire Yb-lineage and has an average evolutionary age 2.39my (Carter et al. 2004). This amplification pattern is similar to that of the Ya-lineage.

reported here, suggest that the first Ya-lineage elements integrated into primate genomes before the divergence of humans and other hominids and that the subfamily remained active in the chimpanzee and gorilla lineages after the speciation for some unknown period of time. However, human-chimpanzee comparisons demonstrate that, at least in the chimpanzee genome, the activity of the Ya5 family has been considerably lower than that of humans (Hedges et al. 2004).

Population Analysis of Polymorphic Loci

Polymorphic loci were analyzed to detect differences in average heterozygosity, genotype distribution and allele frequency between four major human populations (African American, Asian, European and South American). If African populations contain more diversity relative to the other three populations, we would expect the African American population to have an overall average heterozygosity value closer to the theoretical maximum of 0.5. The overall average heterozygosity value for African American, Asian, European and South American populations was calculated as 0.35, 0.32, 0.34 and 0.33, respectively.

For each polymorphic locus, we performed pairwise X^2 "test of independence" tests between applicable, population-specific genotype distributions. The percentage of pairwise tests that showed a significant difference (at the 5% significance level) between genotype distributions were calculated: African American *versus* Asian (45%); African American *versus* European (39%); African American *versus* South American (32%); Asian *versus* European (31%); Asian *versus* South Americans (23%) and European *versus* South American (15%). In order to assess why there were a higher percentage of statistically different African American pairwise comparisons, we extracted the average heterozygosity values from the polymorphic loci that showed statistical differences between the African American population and one of the other three populations then recalculated the overall average heterozygosity value for each population:

African American (0.41), Asian (0.24), European (0.27) and South American (0.26). These values indicate that the African American genotype distributions that were significantly different from other populations were so because they contained a higher degree of heterozygosity.

Materials and Methods

Computational Analyses

Screening of the National Center for Biotechnology Information's (NCBI) Genbank non-redundant human genome database and the University of California Santa Cruz August, 2001 human genome draft sequence was performed using a local installation of BLAST (Basic Local Alignment Search Tool), available at NCBI (http://www.ncbi.nlm.nih.gov/) to identify all *Alu* Ya-lineage elements in the human genome (Altschul et al. 1990). A 16 base pair oligonucleotide **(5'-CCATCCCGGCTAAAAC-3')** that is an exact complement to all *Alu* Ya-lineage elements was used to query the human genome draft sequence. A 700-1200 base pair fragment that included the *Alu* element and adjacent genomic DNA sequences were extracted for individual insertion sites and placed into the University of Washington Genome Center's RepeatMasker Web server (http://repeatmasker.genome.washington.edu/cgi-bin/RepeatMasker) to annotate repeat sequence content as described (Carter et al. 2004). Subsequently, the *Alu* Ya-lineage sequences were aligned using MEGALIGN (DNASTAR V.5) to determine mutation density and element authenticity.

Cell Lines and DNA Samples

Cell lines used to isolate DNA samples were as follows: human (*Homo sapiens*, HeLa ATCC-CCL-2); common chimpanzee (*Pan troglodytes*, CCR-AG06939) pygmy chimpanzee (*Pan paniscus*, CCR-AG05253); lowland gorilla (*Gorilla gorilla*, CCR-AG05251); orangutan (*Pongo pygmaeus*, CCR-AG12256 OR CCR-GM06213); owl monkey (*Aotus trivirgatus*, ATCC-

CRL-1556); spider monkey (*Ateles geoffroyi*, NG053052); green monkey (*Cercopithecus aethiops*, ATCC-CCL-70). Human DNA from South American populations (HD17 and HD18) was purchased as part of the Human Variation Panel available from the Coriell Institute for Medical Research. Additional human DNA samples from the European, African American and Asian population groups were isolated from peripheral blood lymphocytes available from previous studies (Carroll et al. 2001). DNA from the human-rodent somatic cell hybrid panel, used for paralog analysis, was obtained from the NIGMS Human Genetic Mutant Cell Repository at Coriell Institute, Camden, NJ (panel 2).

Primer Design and PCR Amplification

Oligonucleotide primers for the PCR amplification of each *Alu* element were designed using the 700-1200 base pair flanking unique sequence fragments and Primer3 software (Whitehead Institute of Biomedical Research, Cambridge, MA, USA) (http://www.genome.wi.mit.edu/cgi-bin/primer/primer3_www.cgi). The sequences of the oligonucleotide primers, annealing temperatures, PCR product sizes and chromosomal locations for all autosomal Ya-lineage elements can be found on our website (http://batzerlab.lsu.edu). The primers were subsequently screened against the GenBank nonredundant database to verify that they were unique DNA sequence. PCR amplification was performed in 25 µl reactions using 10-50ng of target DNA, 200nM of each oligonucleotide primer, 200µM dNTP's in 1 X PCR Buffer II (AppliedBiosystems, Inc.), 1.5 mM $MgC1_2$ and 1 unit *Taq* DNA polymerase. Each sample was subjected to an initial denaturation step of 94º C for 150 seconds, followed by 32 cycles of PCR at one minute of denaturation at 94º C, one minute at the annealing temperature, one minute of extension at 72º C, followed by a final extension step at 72º C for ten minutes. Phylogenetic analysis was determined by PCR of human and non-human primate DNA samples. The human

genomic diversity associated with each *Alu* element was determined by the amplification of 20 individuals from each of the four populations described above.

DNA Sequence Analysis

DNA sequencing was performed on gel purified PCR products that had been cloned using the TOPO TA cloning vector (Invitrogen) using chain termination sequencing on an Applied Biosystems 3100 automated DNA sequencer (Sanger et al. 1977).

Statistical Analyses

Hardy-Weinberg equilibrium tests using χ^2 "goodness of fit" analysis (using 1 degree of freedom) and a Markov-Chain method (implemented in Arlequin) were performed on polymorphic Ya-lineage elements (Carlo 1992; Schneider 2000). A comparison of Ya-lineage insertion distribution among all human chromosomes was conducted using χ^2 "goodness of fit" tests (using 1 degree of freedom). The expected number of insertions for each chromosome was estimated based on the total genomic sequence that the individual chromosome represented (Arcot et al. 1998). Pairwise χ^2 "test of independence" tests were performed between the genotype distributions of polymorphic elements from four major populations.

Genbank Accession Numbers

The sequences of the orthologous non-human primate *Alu* insertion loci (bonobo, common chimpanzee, gorilla, orangutan, green monkey and spider monkey) have been assigned Genbank accession numbers (AY604157-AY604167) and are available on NCBI's genome nucleotide database.

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CHAPTER FOUR:

SUMMARY AND CONCLUSION

Mobile elements occupy approximately 45% of the human genome. Because of this, they have played a major role in shaping the architecture of the human genome over evolutionary time. The fact that they continue to amplify makes them powerful tools for the study of human genetic diversity, population genetics and comparative genomics. In this work, a comprehensive analysis of the amplification dynamics of Alu Ya5 and L1 preTa elements was performed to ascertain their role in human genomic evolution.

In chapter two, we extracted 362 preTa L1 elements from the draft sequence of the human genome. Estimates suggest that this family contains approximately 400 members in the human genome. Of the elements we extracted, a total of 102 were inserted into other repetitive regions and therefore not amenable to PCR analysis, and 254 were analyzed using a subfamily specific PCR assay. 33 (14%) of these elements were polymorphic with respect to insertion presence/absence across 80 individuals from four geographically distinct populations (African American, Asian, European and South American). About 29% of the preTa L1 elements were full length (approximately 6kb) and twenty nine of the full length elements had two complete open reading frames and therefore may be capable of retrotransposition. Data collected from the L1 preTa subfamily along with the L1HS Ta subfamily (44 elements), yielded a computational estimate of 73 active L1 elements in the draft sequence of the human genome. The estimated average age of this L1 subfamily was 2.34 million years suggesting that their amplification started after the divergence of humans from the African apes. This is also supported by the fact that we did not identify any members of this subfamily in orthologous loci among the non-human primates. The expansion of the preTa L1 elements appears to have occurred over a time frame that predated the radiation of

humans from Africa and has continued until the present. In addition, 28% (100/356) of the preTa elements examined were inverted at their 5' end, which is believed to occur by an event known as twin priming where target primed reverse transcription is interrupted by a second internal priming event. We identified 50 3' transduction events mediated by preTa L1 elements and they have transduced approximately 10400 bases of unique 3' flanking genomic sequence. One transduction event was responsible for duplicating a region of over 1600bp. A total of 12 preTa L1 elements reside within 25 kb of novel or known genes as denoted by GenBank annotation, including one full length preTa element which inserted into intron 23-24 of the retinoblastoma susceptibility protein 1 gene and accounts for 6072 bp of the 7988 bp protein. This vividly illustrates the powerful impact that LINE elements have played in sculpting the human genome and their potential role in the future through continued retrotransposition.

Chapter 3 was a detailed analysis of Ya-lineage of the Alu family of Short INterspersed Elements (SINEs). We extracted 2318 autosomal Ya-lineage elements from the draft sequence of the human genome. A total of 615 of these elements have integrated within repeated sequences and therefore are not amenable to further polymerase chain reaction (PCR) based analysis. Of the 1470 autosomal elements that could be analyzed by PCR, 18 were inserted in paralogous sequences, 1139 were fixed present and 313 (22%) were polymorphic for insertion presence/absence across 80 individuals from four geographically distinct populations (African American, Asian, European and South American). The polymorphic loci were tested to identify differences in allele frequency, genotypic distribution and average heterozygosity. Using this approach we determined that the African American genotypic distributions were significantly different from the

other populations. The Alu Ya-lineage elements were aligned to place them into individual subfamilies. The evolutionary ages of these Ya-lineage subfamilies were then calculated individually and averaged. The estimated age of the Ya-lineage was 2.27 million years. In the course of our studies we identified five non-human primate loci that appeared to contain Ya-lineage Alu elements. However, DNA sequence analysis of these loci showed that they contained older, pre-existing elements from other Alu subfamilies. Thus, these elements are the products of either gene conversions or parallel independent insertions and we conclude that Ya-lineage Alu elements are homoplasy free genetic characters

This research has further established the critical role that mobile elements have played in the evolution of the human genome. We have shown that these elements continue to actively mobilize and alter the landscape of the human genome through insertions, duplications, deletions and recombinations. The research on these two mobile element subfamilies provides a firm foundation for future investigations of the amplification dynamics of L1 elements and Alu elements throughout the primate order. An entire hierarchical series of L1 and Alu elements remain to be identified throughout the primate order.

Future work will include an exhaustive analysis of the mobile element amplification among members of the non-human primates. Previous work suggests that the amplification dynamics of these mobile elements among non-human primates is distinctly different from that of the humans. A complete comparative study of the insertion profiles of these mobile elements in diverse primate genomes may shed light to their significant phenotypic differences that cannot be accounted for at the sequence level. The effects of

insertion and recombination on gene expression would give new insight on the overall role of these elements in the evolutionary process. The potential for groundbreaking discoveries in mobile element biology and the effects of their propagation could lie in the genomes of these primates. These studies would further provide numerous new genetic markers for the study of primate phylogenetics, population genetics and evolution.

Our research on these two subfamilies of L1s and Alus did not identify any elements that have inserted in open reading frames and that may be associated with disease phenotypes. But our results indicate that these elements continue to mobilize and their potential to cause disease through insertional or recombinational events is patently clear. They also have a role to play in the continued evolution of the human genome. They may have established a state of nearly complete neutrality by compensating their hosts with selective advantages, thereby driving their success. This can be seen in the proposed role of L1s in X chromosome inactivation and genetic imprinting, L1s and DNA repair of double stranded chromosomal breaks, the proposed role of retrotransposon reverse transcriptase on eukaryotic cells acquiring telomerase activity, the role of Alus in alternative splicing and segmental duplication and other examples. There are also certain research applications of L1 element biology that hold great promise. Due to their weak target site preferences, L1s amplify relatively randomly in the genome and this is very attractive for use in a random mutagenesis system especially in mouse genetics. The L1 element and its ability to transduce unique genomic sequence can potentially be used as gene delivery vehicles in gene therapy.

In conclusion, the overall effect of these mobile elements in the evolution of the human genome has not been comprehensively elucidated. There is a lot more to be

discovered, and this research is a small part in our attempt to understand and appreciate the role they have played over evolutionary time.

APPENDIX A:

LETTERS OF PERMISSION

6 January 2005 Our Ref: HG/jj/Jan05/J120

Anthony C Otieno
Graduate Student
Louisiana State University
107 Life Sciences Building
Baton Rouge LA 70803
USA

Dear Anthony C Otieno

JOURNAL OF MOLECULAR BIOLOGY, Vol 342, No 1, 2004, pp 109-118, Otieno et al: "Analysis of the human …"

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Yours sincerely

Helen Gainford
Rights Manager

ELSEVIER

6 January 2005 Our Ref: HG/jj/Jan05/J156

Anthony C Otieno
Graduate Student
Louisiana State University
107 Life Sciences Building
Baton Rouge LA 70803
USA

Dear Anthony C Otieno

JOURNAL OF MOLECULAR BIOLOGY, Vol 3326, No 4, 2003, pp 1127-1146, Salem et al: "LINE-1 preTa …"

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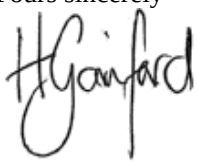

Helen Gainford
Rights Manager

APPENDIX B:

SUPPLEMENTARY DATA

Table 1. PreTa L1 primers, PCR Conditions, and associated human genomic diversity

Name	Accession	Chrm. Loc.[1]	Forward Primer	Reverse Primer	Human Diversity[2]	AT (F,R)[3]	AT (ACG)[3]	PCR Product Sizes[4] Filled	Empty	Subfamily Specific
L1AD1	AC080166.6	2	AATTCGCTGCATAATTTCTT	AAACATATGGCCATCTTGAC	FP	55	60	6835	249	578
L1AD2	AC090955.2	3	TTTTCTCCATGACTTGAGATGGT	TGCAATCATGAAAACCAGTG	FP	60	60	6308	245	265
L1AD3	AC018878.8	2	TGCACATGGATGTGTAAGAATAC	TTCTTCCCATAAGCATTGGT	FP	60	60	6448	339	245
L1AD4	AC053545.5	4	TTGATGCATTTCTGCATAAGG	CCAAGATTTTGGCTAGCATTT	FP	55	60	4528	295	188
L1AD5	AC079801.2	16	TCATCTCACAGAGCTCACAG	CTAGGAATCCTTCTGTCTGG	NP		60	749	326	150
L1AD6	AC073647.9	7	GCAAACACTGGTTCAAGAAG	TGGAGATAGTGTAGGCACAG	FP	55	60	1741	87	233
L1AD7	AC093607.3	4	INSERTED IN REPEATS		R					
L1AD8	AC079926.7	4	GCCTCTTTCTTAGTCAAGCA	AGGTCACAAGGGACATTTCT	NP		60	857	417	208
L1AD9	AC012593.8	2	CAGGTAGGGGAAAGGAGGAG	TGGGCTTATTATCCCCTTGA	FP	55	60	1034	392	342
L1AD10	AC016906.7	2	TGTATTTACCGGGGATGAGG	GCTGTCCCAAATTTCCAGAG	IF	60	60	3602	172	229
L1AD11	AC018465.8	2	GCACCTTGCTATTTGTTTTCT	CCCTAGAGCAATCACCAAAGA	FP	60	60	6515	458	185
L1AD12	AC083950.4	2	GGATAGGCAATGTGTTAGGT	TGCAGAGGCAGTTGTAACAT	FP	55	60	1106	603	303
L1AD13	AC097484.3	4	AAACCTATACATAGAAAATTGCTG	ACCCAGAACAAATGAACACT	FP	60	55	1368	473	424
L1AD14	AC012665.8	2	TTCTGCAACTATAGCCGTAA	ACAACAGACACAGAAGCAAA	IF	60	55	6187	136	173
L1AD15	AC093584.3	4	INSERTED IN REPEATS		R					
L1AD16	NG_000004.1	UNK	GGTTGAGAACCACTGTCATAA	GCCAGTGCTTAGATTTACCA	FP	60	60	6213	145	260
L1AD17	AC105459.1	7	ATTCCCCATTTTACGATTTT	GCTACTGCCGTGTTTTACA	FP	55	60	440	276	309
L1AD18	AC096764.3	2	AGATGCCCGGTCTACTACTT	AGCACTTTAAAGGCATCAAC	FP	55	60	3467	151	249
L1AD19	AC009156.9	16	ATATTGGCCAAAGCCTCTTA	TGGCAAGTCCTGAATGATAA	IF	55	55	3974	88	191
L1AD20	AC009156.9	16	CATTAGCAAGCTGATTCAAA	CTTTTGCCATGATTAGTGGT	HF	55	60	474	147	205
L1AD21	AC097522.4	4	CAGAAAGTCATCTCATCTTCC	TAAAGCATTCGTTGTTGTTG	FP	55	60	6528	353	587
L1AD22	AC092570.3	2	CCTCCTCACCTCCTTTTAAT	ATGAAGGGAAACGAGAAAAG	FP	55	60	562	63	220
L1AD23	AC018673.4	12	INSERTED IN REPEATS		R					
L1AD24	AC097451.2	4	TCGTTCCTCATCTCTTTGTT	AGCAAAAGCAGTCACTTTTC	FP	55	55	3467	382	396
L1AD25	AC023154.5	4	INSERTED IN REPEATS		R					

L1AD26	AC096769.3	4	TTGAGTTTTCCCTCCATGAAA	TCTGATGAATTGTGCCTGACA	FP	60	60	381	157	263
L1AD27	AC093877.3	4	AATATTTAACATGGCCCATAA	GGCATTGGTGTCAATGAGAA	FP	60	60	1171	110	834
L1AD28	AC096749.2	4	GAAGGCTTTATACTCCTTCTTGGA	TCATGGGAGATTTTTCAACTTTC	FP	55	60	6459	419	330
L1AD29	AC105150.2	8	GGACAGAAATACTGGCATCT	CACAATCTTATCTCAAGGGAAT	FP	60	60	6398	318	354
L1AD30	AC055820.7	18	CTTGATGGCAATACAGCCTAA	CCATTAATGTGGGCTCATAATCT	FP	60	60	1855	78	208
L1AD31	AC018626.8	18	GGGAAACGACAGAAGATGGA	GAATTTTGATTTGTGGGCATA	FP	60	60	1143	209	204
L1AD32	AC091613.3	1	END OF CONTIG		EC					
L1AD33	AC092798.3	3	INSERTED IN REPEATS		R					
L1AD34	AC012642.5	5	GGCTTGTGCTACACAGAGTT	CCAACCAGGAACAATAAAAG	FP	55	55	2816	519	247
L1AD35	AC021538.8	UNK	AAATGCCCACAAAATTCCTG	CCATGGGAGCTACTGGAAAA	FP	55	60	984	386	479
L1AD36	XM_037013.1	UNK	END OF CONTIG		EC					
L1AD37	AC099515.2	5	INSERTED IN REPEATS		R					
L1AD38	AC026703.4	5	CCCAGTTCTCCAAAATATCA	CACTTGCCTATGGTTCATTT	FP	55	55	5984	240	468
L1AD39	AC078857.12	3	INSERTED IN REPEATS		R					
L1AD40	AC078857.12	3	TCGTGACCTTATTAGCCACT	CCTCCATTTGCTACCTAGAG	FP	60	60	1680	512	633
L1AD41	AC078857.12	3	TGTTATTTCAGCTTTAACCATCAA	TTTAAAAATCAAGTATGGGAAAAA	FP	55	55	1202	141	242
L1AD42	AC093515.3	16	INSERTED IN REPEATS		R					
L1AD43	AC011597.27	3	INSERTED IN REPEATS		R					
L1AD44	AC079943.18	3	ATGCCATCCCCTGGATTT	TGGTTGCTCCAAAGGAACTT	NP		60	6591	530	316
L1AD45	AC061710.16	3	GAGCAAATTTGTCAGACAGAACA	TGGGATGGTTGAAATCAAATG	FP	60	60	3854	147	199
L1AD46	AC072051.8	UNK	CCCTATTTTCCCCATCATCA	AAGCAGGCAGATGGTCACTT	FP	55	60	3706	69	166
L1AD47	AC008006.10	18	CGTCACACACATAACCAGAG	GATCAGGAATATGGCAAAGA	FP	55	55	471	212	284
L1AD48	AC027553.6	UNK	TGCATGAAGCACTACTCAAAGA	TGCAAGATGTGTCAGTATTTAGC	FP	60	60	6181	106	226
L1AD49	AC018991.10	UNK	INSERTED IN REPEATS		R					
L1AD50	AC008948.8	5	INSERTED IN REPEATS		R					
L1AD51	AC008728.7	5	INSERTED IN REPEATS		R					
L1AD52	AC093566.3	8	INSERTED IN REPEATS		R					
L1AD53	AC020783.8	8	INSERTED IN REPEATS		R					
L1AD54	AC068062.5	10	CCTTTGTTTCTTGGGTGTGG	CCCACATCACCAAACCATTT	FP	60	60	357	128	212
L1AD55	AC064875.5	2	GCCACACTCCTTTGTTTGCT	CAAGCACAAAAGCAGGAACA	FP	60	60	724	193	273
L1AD56	AC073275.8	7	INSERTED IN REPEATS		R					
L1AD57	AC010747.10	2	CGGAAAATTTGTTACTTGCT	AGGTATGCTGCATTTCTTTC	FP	55	55	3903	97	272
L1AD58	AC012509.13	2	CCCTGGATGCTGAGTTTCTT	TCCATCTGGCATTGACTCAG	FP	60	60	1062	139	213
L1AD59	AC009964.11	2	TGGGACATTGACTCCTACTC	GGCATAGGTTTCTGGAAGTA	NP		60	760	340	282

L1AD60	AC009961.11	2	INSERTED IN REPEATS		R					
L1AD61	AC078851.4	2	TTTATGCTGATCACTGTTCTTC	AACTAGTTGCATCGTGATCATA	FP	60	55	2090	80	208
L1AD62	AC016720.9	2	CTTTCGCATCATCGTAAAGT	ATTGCCAACTGGTTACAAAG	FP	55	55	2886	114	261
L1AD63	AC012492.9	2	AAAAACCCTTTAAGCTCAGT	TGGAAGCATACAAAATGAAA	FP	55	55	6402	342	180
L1AD64	AC069285.8	7	GCCACTGCTAATCAATTCAC	CCAAAGCAGACACAATTTCT	PARALOG	55	60	6131	77	172
L1AD65	AC026029.8	4	TTTCCTCAAAGTTGATGCTC	CCTGGAAGGCATAACTGATA	NP		55	6787	271	575
L1AD66	AC025223.6	2	TATCCAAATATCCCTTGCAG	TTGTAGTTTGTGGAACTGGA	PARALOG	55	55	717	201	197
L1AD67	AC095347.6	12	INSERTED IN REPEATS		R					
L1AD68	AC069242.13	3	CCTATGGATGAAAAATGGAC	TCTGAAAATGTTGCCATTG	FP	55	55	294	111	176
L1AD69	AC092325.2	16	INSERTED IN REPEATS		R					
L1AD70	AC079841.10	3	TCCAAGAGCAGGCAGTATTA	TTCCTGACTACTCCAGTTCAG	FP					
L1AD72	AC092468.9	3	GTGCAGGTGTAAGGAAGAAA	GTCTTCAAACCAGACTGCAT	FP	55	55	546	93	218
L1AD73	AC097657.3	4	TGATTTGCAGTATTTTTCCTT	GCATGACCCAGATTAGAAAA	FP	55	55	1148	126	168
L1AD74	AC097463.2	2	NO RESULTS		NR					
L1AD75	AC092018.2	1	TTTCTCTCCCTCAAGCCTTTT	CCAAAATTCATGCTGGGAAC	IF	60	60	1636	129	124
L1AD76	AC027345.5	4	AAACCTCCCTTTAGTCTCCA	CACCAGACCCAATTTTTAGA	FP	55	60	4500	221	173
L1AD77	AC097110.1	4	TCAAGGAAGGGAGTTAAAAA	ACTTCTTTCATGCCCCTTAT	HF	55	55	991	729	237
L1AD78	AC026439.4	5	TCTTGAGGCTTGCAAATACT	ATGAGCAACAAGAAATCACC	FP	55	60	1559	295	306
L1AD79	AC016620.7	5	INSERTED IN REPEATS		R					
L1AD80	AC092185.3	3	AAGCAGTATGTCTGGCACA	ACAAACTGACACTCCAAACC	FP	60	55	6148	72	197
L1AD82	AC022165.8	16	GGTGTCTCCACAGTTGATTC	CCACCGCCAGATTTTACTA	HF	55	55	2876	117	196
L1AD84	AC090525.8	12	TTCCCTGGGTCACTTTTCTC	TGCCAAATTGCTTTGCATAC	FP	55	55	2068	255	333
L1AD85	AC026120.33	12	INSERTED IN REPEATS		R					
L1AD86	AC093865.2	2	ACATGATGTCCCATCTTCCA	AAGAGCCATATGAGAGCTTCC	FP	60	60	1046	271	304
L1AD87	AC022446.6	5	AATTTTTCCCCACATGTTC	ACAGAATGGATTTAGCTTGC	FP	60	60	3761	118	248
L1AD88	AC090519.3	15	INSERTED IN REPEATS		R					
L1AD89	AC084819.17	12	INSERTED IN REPEATS		R					
L1AD90	AC092601.3	2	INSERTED IN REPEATS		R					
L1AD91	AC008571.6|	5	TGCTAAACAGAAGGCACATA	ATAGATCCATCTGCCAAATC	FP	55	60	6266	170	314
L1AD92	AC092638.2	2	TTATCCAAAGAAGGGGAAAGG	TTTGCCTTATAAGCATTGTGAAAA	FP	55	55	6224	181	195
L1AD93	AC096653.1	4	CAACACTCATTACAACCTGTG	CAGAGTTTATCAGCCAGACC	FP	60	60	2336	382	399
L1AD94	AC092581.2	4	CTCCACGTTAACAGATAGGG	TGAGCTTCACTTAACCACTG	FP	60	60	507	341	239
L1AD95	AC096569.1	2	CCAGCACTGATTTCATAGATGC	TTCAGACAACTGAAGTGCCTTT	FP	55	55	6161	89	224
L1AD96	AC092631.1	4	TAATTAGGTAACGCCTGTGG	CAGGAAGCCTAAACTGCTT	IF	60	60	932	98	245

L1AD97	AC008709.6	5	CCCCAGGCTTTTGAAAATTA	ATTCTCGGGGTCCCAATTAC	FP	60	55	6164	111	214
L1AD98	AC060796.7	17	ATGGAAAGGGGAAGATTTTA	GGCTATACTACAACATCCCTCA	FP	55	55	6164	126	203
L1AD99	AC090791.6	11	GTGACACAAAAAGCACAATTAC	CAATGATTCATGAGTTGGAA	FP	55	55	2737	292	303
L1AD100	AC026729.5	5	CCTGGGTCACAATATGAAGA	TCTGATAACCAGAAGATGAAGA	HF	55	60	6324	258	352
L1AD101	AC025467.5	5	AGTCTCCCTTTCAGAAGCA	AATGCTGGGAATCTTACCTC	IF	55	55	6091	66	163
L1AD102	AC025467.5	5	GAATGGGGTGTGCTGTAA	TTTTAACAAGATCCCAGACC	IF	60	55	3721	78	164
L1AD105	AC010275.6	5	ATTCTCGGGGTCCCAATTAC	CCCCAGGCTTTTGAAAATTA	FP	55	55	6164	111	214
L1AD108	AC008550.5	5	CACAATCATACCTTCCCAACTG	CAGATGAGACTTTGGACGTGA	FP	60	60	6154	84	187
L1AD110	AC092721.2	16	ATTTTGTGGTTCAGCATTTT	CATAGAAAAGGGAACAAATGA	FP	60	60	1590	82	226
L1AD111	AC092357.2	16	AAAAGTTGTTTTCCTGATTTTT	AGTTTTCTCTGCAGCTCATC	FP	56	55	6252	188	184
L1AD112	AC034219.5	5	TTTCCAAAAACAGCTAGGAG	CGTTTTTCTAGCTTAGCAATG	FP	55	55	406	106	209
L1AD113	AC005406.2	UNK	ACCTTGATTGCAAATTGTTT	GGTTTCTTGGCCTCTTTACT	FP	60	60	2881	80	189
L1AD114	AC020651.19	3	INSERTED IN REPEATS		R					
L1AD115	AC084032.23	12	AACTGCCATGAAAACTTACC	AAAGATTGTCCACATCAAGG	FP	55	60	253	100	190
L1AD116	AC025176.5	5	END OF CONTIG		EC					
L1AD117	AC022024.6	10	CAGCAACCATAGGTTGATAAG	GGATTACTGCCCAAAGAAAC	FP	60	60	852	487	310
L1AD118	AC026113.25	12	GACTGCTGGATCAAATGTTAG	ACCACCTTACTCCTGCTACA	R	55	60	6231	188	272
L1AD119	AC024941.30	12	CTTTATTCATGGCAGAAAGC	CTCATGAGATCTGGTTGTTT	R	55	60	1347	112	249
L1AD120	AC066613.7	UNK	INSERTED IN REPEATS		R					
L1AD121	AC010857.8	4	INSERTED IN REPEATS		R					
L1AD122	AC011712.6	18	CCCAGGGGAATATATGGAAATTA	AATTGAATGCAGATGGTTTTACC	FP	60	55	6631	139	608
L1AD123	AC010928.7	18	CCAGGAGTCAGAGGATTACA	TCTGTTGTGAGAAGCAAATG	FP	60	60	410	98	172
L1AD124	AC013759.6	18	INSERTED IN REPEATS		R					
L1AD125	AC013759.6	18	AAACGGTGAAGGAAATGTTG	GACATGAGCAACCATCAGGA	IF	60	60	513	236	309
L1AD126	AC021082.4	5	INSERTED IN REPEATS		R					
L1AD127	AC012323.7	16	INSERTED IN REPEATS		R					
L1AD128	AC025097.41	UNK	INSERTED IN REPEATS		R					
L1AD130	AC039057.8	UNK	INSERTED IN REPEATS		R					
L1AD131	AC073258.9	7	INSERTED IN REPEATS		R					
L1AD132	AC017014.4	2	GGGAAGTGAAGGCTAACATA	ACCATGGAGCTCAATTTACA	FP	60	60	469	84	187
L1AD133	AC069294.5	7	GGTTGAGAACCACTGTCATAA	GCCAGTGCTTAGATTTACCA	FP	60	60	6212	145	259
L1AD134	AC084732.1	4	CTACCCAGAACAAATGAACAC	AACCTATACGTAGAAAATTGCTG	FP	60	60	1368	475	422
L1AD135	AC008276.4	2	CTCAAGGGTTCTCATCACTAA	GGAAAGGATACCACAATCAA	HF	60	60	1871	87	191
L1AD136	AC017015.4	3	TGGCTGACAAATTGGTGATT	CCCATGTGAACTGCATTGAA	FP	60	60	712	293	217

L1AD137	AC010970.3	Y	INSERTED IN REPEATS		R					
L1AD138	AC012284.5	15	GAGCTGAAGAAACAAAGGAA	ACCTCAAATTCATTTTGGAA	FP	55	60	780	75	200
L1AD139	AC009479.4	Y	INSERTED IN REPEATS		R					
L1AD140	AC010722.2	Y	TTCAGGAACATTGCTATGAGGAT	TAGGCATTTATCATGTGCTC	FP	55	55	1643	218	283
L1AD143	AC079175.24	X	CAGTAAACTGGGCTGCTATC	GAGAGTCAAGCAGTGGGTAA	FP	55	60	5078	80	208
L1AD144	AC023842.5	8	CACAAGATTCAATACCTGAGTGACA	TGGGCATTACTAGTTGAACCTAAAG	FP			1641	141	261
L1AD145	AC087883.12	12	GAAGGAAGCCCCCATATGAT	GAGGTGAAAGGCCATTAAAGAA	FP	60	55	473	147	243
L1AD146	AF280107.1	UNK	END OF CONTIG		EC					
L1AD147	AC063951.22	12	END OF CONTIG		EC					
L1AD148	AC024060.5	3	AACTTCCTTAGGACCTCATTT	TGTGTTTAACGTTCTAAACCTG	FP	60	60	1361	65	229
L1AD149	AC087433.4	15	CCGAAACACAGATAAGCACT	AGTGTAAAAATCTGCATAGCC	FP	55	55	2160	508	274
L1AD150	AC073572.19	12	ATTCCCCCAATTCTCCAAAA	GCAAGGGCCAACTATGCTAA	FP	55	55	1195	124	187
L1AD151	AC023795.18	12	INSERTED IN REPEATS		R					
L1AD152	AC079865.14	12	GGGAGATCCAGACATACAAC	TGTGTAACTCTTTTGCGATG	FP	60	60	569	369	341
L1AD153	AC058784.17	13	INSERTED IN REPEATS		R					
L1AD154	AC023812.7	3	ACCTCTACCTTACCACACCA	CCTAACTCAGGTCATTCTGC	FP	60	60	1475	175	260
L1AD155	AC018923.21	3	INSERTED IN REPEATS		R					
L1AD156	AC008436.5	5	INSERTED IN REPEATS		R					
L1AD159	AC008496.5	5	INSERTED IN REPEATS		R					
L1AD160	AC034194.4	3	AGAGCTACATGGCTAAATGC	TCTGCAGTTTTAACACCTCTT	IF	60	55	543	238	261
L1AD161	AC011546.6	19	INSERTED IN REPEATS		R					
L1AD162	AC020717.3	X	TTCCTATAGGCTTGAATGGA	TTTTGGTGCCCAATAGTATC	FP	55	60	2923	198	219
L1AD163	AC007132.3	2	CCCAGTATGTCCCTCACTCAG	TAGGCAAACCCCAATTGAAA	FP			6359	315	351
L1AD164	AC006968.2	X	TTCCCTGTCCAATGTAAAGAA	AAAGTGCATATTGCACAGGA	FP	55	55	836	107	158
L1AD165	AC010685.3	Y	INSERTED IN REPEATS		R					
L1AD166	AC010889.3	Y	CCCTAACATTTCAAAATGCACTG	ATTTTTCCAACTACTGGCACTCA	FP	60	60	1256	162	214
L1AD167	AC006334.3	7	INSERTED IN REPEATS		R					
L1AD168	AC009489.3	Y	TGCCTTTATAATATGGAAATGCAG	TGCTCATGGAGTCAGAATATGAA	FP	55	55	1080	196	183
L1AD169	AC011745.4	Y	TCCCATTGCATTTAGCAGATT	AGGCCTGTATTTCAATTGTGCTT	FP	60	55	3676	95	265
L1AD170	AC007278.3	2	GTCTATTAATCCCCCTCCAC	CAACGTTGAAAAGATGTAGAGA	FP	60	52	6149	87	174
L1AD171	AC006992.2	7	TGGAACTATTTCAGGAAATTAAA	AACAAGGGGGAAGAGAATAA	FP	55	55	6278	197	234
L1AD172	AC006362.2	7	INSERTED IN REPEATS		R					
L1AD173	AC015542.17	3	TTCCAATATACTTTGCCCTTA	AGTAGGCATCAGCAACAGTC	FP	55	55	546	393	322
L1AD174	AC022013.3	3	TTTGGGGAGAACTATCTGTG	GCTTGGACATTGGAATTTT	FP	60	54	399	118	188

L1AD176	AC026204.4	3	GCACTCTCATTTACTGCTGA	CCACCTTTTACTATTTTGGTG	IF	60	55	838	494	195
L1AD177	AC018514.7	14	ACCAGATGGAAGCTAGATGA	AAGTTTCCAAGGGAAATCAG	FP	60	55	6370	256	373
L1AD178	AC058791.3	7	ATTGTTTAGGGGAAAAGGAC	CCAAAAGCAGGTTAATTCTC	FP	55	55	629	203	322
L1AD179	AC013738.4	10	ACTCCACTTTAATTCGCAAG	GAAGGCGAGAAACTGTAGAA	FP	55	60	1056	113	289
L1AD180	AL627250.8	X	INSERTED IN REPEATS		R					
L1AD181	AL449304.19	9	TTCCATAGCCATTGATTACA	AATTTTCAGGCACGTTTTTA	FP	55	55	652	286	446
L1AD182	AL137787.11	X	INSERTED IN REPEATS		R					
L1AD183	AL445312.5	X	GTCCAGAAGTCTCTCCTGTT	CGATTGCAGGCTTTCTAATA	FP	55	60	2873	105	413
L1AD184	AL360020.15	9	INSERTED IN REPEATS		R					
L1AD185	AL391260.13	10	TTCTGTAGGGCTCCTGACTA	ATTCACAGTTCCCCGTAGTA	FP	60	55	7905	185	1829
L1AD186	AC016951.9	3	ACTTGAAATTGGGGTAGATG	ATTTTCTAGAGGGCTCCTTG	IF	60	59	843	190	206
L1AD187	AL365258.24	1	INSERTED IN REPEATS		R					
L1AD188	AL603765.6	1	INSERTED IN REPEATS		R					
L1AD189	AL596326.5	1	TGTTTCATGGAGTGTATTTCA	TGCAATGTTAGAAGAAGTGG	HF	55	55	456	198	289
L1AD190	AL606752.11	1	GCTTGACACATAGTGCTTGA	AAATGTGGCATTATTTTCACT	FP	60	60	462	250	193
L1AD191	AL589877.13	X	ACCCAGAAACGCATATACAC	GCAAATTGCAACAAGATAAA	FP	55	55	1926	591	352
L1AD192	AL513493.11	1	TGTCCAATTAAAAGGCACAT	TGGAATATCTTTTTCTGCCTA	FP	55	60	941	134	322
L1AD193	AL359733.15	1	TCTTTTACTCCCAAAAGGAA	TTGGGTAGATGAAGATGACC	NP		55	1900	260	292
L1AD194	AL357873.17	1	GCCCTGGATGTAGTGTATGT	CTCTCTCTTCATCCGTTCAG	FP	55	55	974	144	256
L1AD195	AL592494.4	1	NO RESULTS		NR	55	55			
L1AD196	Z82209.2	X	TTCTCTCCTAACCCTCTTGG	TTTAGGGTATGCGGTAGAAG	FP	60	55	6581	349	385
L1AD197	AL354949.10	1	GAAACTGAGATTCACGGAAG	AGTTTCTCATCCCACCTTCT	FP	60	60	6437	360	467
L1AD198	AL138785.8	1	GCTTCACCTCACTAGCCTTA	CTCACAAAGCAGCATTTACA	FP	60	60	456	87	163
L1AD199	AL445197.4	1	TTCAGCATATCTGCAAAGTG	GAAAGGATTCTCATTTCCTG	FP	55	60	626	216	341
L1AD200	AL136224.24	6	CAGTCTATCAATTCCTGTTGG	TGATCATCCAGCTCAATTACT	FP	60	55	2353	472	440
L1AD201	AL607144.5	13	CAGACTTGGGCATCTTTTAG	AAAACATCAGGGCCAAATA	FP	55	57	1328	148	178
L1AD202	AL513324.8	10	INSERTED IN REPEATS		R					
L1AD203	AL390834.24	10	INSERTED IN REPEATS		R					
L1AD204	AF245226.1	21	INSERTED IN REPEATS		R					
L1AD205	AL596342.3	1	GACTCTTCCCCTTGAGAATC	GCATGCCTACGATCTCTTAT	FP	55	55	381	222	253
L1AD206	AL603902.4	6	INSERTED IN REPEATS		R					
L1AD207	AL592067.4	13	ATTTAGGTATGCGTTTCAGC	ACATCTCTTCATGCCTTCAG	FP	55	55	999	422	238
L1AD208	AL353743.22	9	ATCTCCTATCCCCTTAGCTG	AACCCAAGAGTCACAGTTGA	HF	60	60	1978	530	280
L1AD209	AL139282.10	1	TTGAGTCAAGGAAAAATAATGA	AAAGCAAGGCAGGTATGTTA	FP	60	60	1667	214	245

L1AD210	AL512504.9	X	INSERTED IN REPEATS		R					
L1AD211	AL590439.12	10	ATATTGATTTGGCATCCTGA	GTAAACGTTCTAGCCAAAGC	FP	60	60	6207	155	169
L1AD212	AC007347.3	16	CACGGGAGAAGATTTATGTC	TTGTACCTACTCCACCCAAG	FP	54	55	6400	210	310
L1AD213	AC007262.4	14	GCCATAAACAGAAAACCATT	GTTGCAGAAATAACAGCACA	IF	60	60	494	182	294
L1AD214	AC007221.2	16	GCAGTCAACATCTTCCAGTA	TGAGCTAGAATCCCAAAGAT	FP	55	60	6267	135	324
L1AD215	AC007115.1	12	TGAAGAACCTTCACGTAAGAA	AAATATGATGCTTTGCTTCC	FP	60	55	556	176	362
L1AD216	AC006143.1	X	GAGGCTTACTGGAAGCATAG	CTCACGGTTGATGTCACTTT	FP	60	60	1494	430	520
L1AD217	AC011594.8	12	CTGGCCAAAGAGGTAGTTT	CAAAAGAGCATGGTACTGGT	NP		55	7620	479	537
L1AD218	AC004141.1	7	TCCTTAACCTAGTTGCTCCA	AGGGTACATTGAAGTTGAGG	NR	60	60	624	340	458
L1AD219	AC002076.1	7	AGGGAATATTTGGGACATCT	CCCCACCACACTAGAAACTA	IF	60	60	6418	354	391
L1AD220	AC003085.1	7	CCAGGGAACTTGATTTTAGA	CAATTGGATAAGAGGGACTG	FP	60	55	6500	303	199
L1AD221	AC004161.1	UNK	INSERTED IN REPEATS		R					
L1AD222	AC006204.1	7	TTTGGAAGCTTCACTTTAGC	TGGCCTTAATATTTTAGCAAC	FP	60	60	590	167	246
L1AD224	AL356096.11	13	INSERTED IN REPEATS		R					
L1AD225	AL513355.16	10	CGGTTCTAAACACCATTTGT	TTATGGCCCTTAATTTCATC	FP	60	60	1739	177	192
L1AD226	AL358873.25	6	GCATCTTTGAATCAACAAGTC	TGTATCTAACTATTCCCAGTGATT	FP	60	55	986	238	751
L1AD227	AC004822.1	X	TTGAGAGCATCCATATTTCC	CCAACCTCAGATTACCAAGA	FP	55	60	768	115	202
L1AD228	AC005053.1	7	INSERTED IN REPEATS		R					
L1AD229	AL450312.10	9	INSERTED IN REPEATS		R					
L1AD230*	AL583806.7	6	GCAATCCATAGACAACCAAT	AGGAGGAATATGCAAACTGA	HF	55	55	2249	599	338
L1AD232	AL583825.8	1	TCCCAGAACTACCTCATAACA	GAGGAAGACAGTGTCACAGA	IF	60	60	1162	219	329
L1AD233	AF207955.1	21	AGGGGTAGATTTTGTTCAGA	AGGACCATTTGCAATGTTAG	FP	60	60	1283	747	667
L1AD234	AL391992.8	10	TGGCTAGTCACCCTAAAAGA	GTTTTATAGGCTTGCATTGG	FP	60	55	6487	388	360
L1AD235	AL160234.3	14	GGAGCTATTAAGCCACAAAA	GAGAGGGTATCCTCGTCTTA	FP	55	60	6771	694	326
L1AD236	AL079307.7	14	GAATGGGGAATTATACGTGA	GTAAGGCACTTGGAAATGTG	FP	60	60	6260	196	295
L1AD237	AL162431.17	1	AAGTGAATGTGGATTTACCC	TCTCAAGGAAATCAGCTCTT	FP	60	60	6499	435	324
L1AD238	AL389895.3	14	ACTTTTATGCCTGAAACCTG	ATCCTTTCTCAGAGGGATCT	FP	60	60	6370	325	278
L1AD239	AL357045.10	1	INSERTED IN REPEATS		R					
L1AD240	AL591770.1	14	GTCTCAGACACACAAGCTCA	TTGGCCACTCATCTATCTTT	HF	60	60	540	222	258
L1AD241	AL512310.3	14	INSERTED IN REPEATS		R					
L1AD242	AL136960.4	13	CCCCTGAAGAGTCCATATAA	CCTAACAGTCAGGAAAGCTG	FP	55	55	6347	288	197
L1AD243	AL445466.9	1	CTGCTTGTCTTTGGTCTGAT	GTGATCCTGTAGGCCTTCTT	FP	60	60	2933	410	1229
L1AD244	AL512790.1	14	GCATCCGTTTCTCTGATG	TGCAGATTGTACAGAAAAGC	FP	60	60	1394	166	296
L1AD245	AL136295.3	14	ACTTTAGGATTCCGTGGTTT	AATGCTGTTAGAGGAGGATTC	FP	55	60	2193	482	222

L1AD246	AL391838.9	13	INSERTED IN REPEATS		R					
L1AD247	AL512662.8	UNK	INSERTED IN REPEATS		R					
L1AD248	AL138694.18	UNK	INSERTED IN REPEATS		R					
L1AD249	AL133241.3	14	INSERTED IN REPEATS		R					
L1AD250	AL121852.3	14	CCCTCAAGAACGATTTTATG	TGTCTAGAATGTTCCCCTTT	FP	60	60	6397	280	237
L1AD251	AL117191.6	14	CTGTGGAGGAAACATTGAAG	TCACACTCAAAGACTCCTTTC	IF	60	60	1995	172	288
L1AD252	AL590370.2	6	GTGAAGGGCACTGGTTATTA	TAATGAAATCGGACCTGTCT	FP	60	60	6498	408	202
L1AD253	AL163613.2	14	TTGCCTAGCTTTTCTACCAG	TTCAAGCTACCTTCTCAAGC	IF	60	60	1369	726	180
L1AD254	AL118557.5	14	ACCTTGACATTCCTGCAA	AATCCACCTGCAGACATTAC	FP	60	60	1000	143	514
L1AD255	AL117693.5	14	TCATTGTTCTATCCATGCCTTTT	GTAGGTTTGGGGCTGGAAAT	IF	55	60	961	197	228
L1AD256	AL161804.4	14	INSERTED IN REPEATS		R					
L1AD257	AL359545.12	10	INSERTED IN REPEATS		R					
L1AD258	AL358293.4	14	GGTTCAATTGAGCGTTACTT	TGCTGATATAGCACCTAGCA	FP	60	60	6800	735	300
L1AD259	AL158111.5	14	INSERTED IN REPEATS		R					
L1AD260	AL133238.3	14	GGTGGATGTATCCATTGTTT	TTTATGCATGCAAGAAATGA	FP	55	55	627	436	464
L1AD261	AL049838.3	14	CTATGGACCCATCTGACTGT	AGTTATTAAACCGGCCACTA	FP	60	60	6269	222	245
L1AD262	AC006568.7	4	ACACGGAGACACTTCAAATC	ACCCGTTATTGTGTTCAGAC	FP	60	60	6424	363	407
L1AD263	AL355481.12	13	GGCTACTTTGGCTTCTGTAA	ATTTGCTCAAACATTTCTGG	FP	55	55	5616	511	531
L1AD264	AL031681.16	20	GGGGAAGTTCCTCCTATATT	AAATGGTAGGTTGGTTTATCA	IF	60	60	1699	501	350
L1AD265	AL589693.3	6	ATAAATTTTCAGGCCTTTCC	GAACAAATTAGACACCATAAGGA	FP	60	60	6218	172	189
L1AD266	AL365508.19	6	INSERTED IN REPEATS		R					
L1AD267	AL445258.4	X	INSERTED IN REPEATS		R					
L1AD268	AL034425.9	20	GTTTAACCCAGCTGTCCAT	TCCTGTCTCATTTGCTTACC	FP	60	60	2022	361	395
L1AD269	AL136090.12	20	TGACATGGGAGCAATAATAGT	CAGGTGAAATGTATTGAAGGA	FP	55	55	1933	315	371
L1AD270	AL135936.11	20	INSERTED IN REPEATS		R					
L1AD271	AL390057.12	6	INSERTED IN REPEATS		NR					
L1AD272	AL161901.18	13	INSERTED IN REPEATS		R					
L1AD273	AC006947.2	17	GCCTGCTACATGTTCAGAT	CCATCCTTTCTGGAGTGAT	FP	60	60	6252	214	243
L1AD274	AL161938.6	20	INSERTED IN REPEATS		R					
L1AD275	AL157380.15	X	INSERTED IN REPEATS		R					
L1AD276	AL031679.1	20	ATTCTTCCTGCCACCTTATG	TTAATAGCTGAGCATCATGG	FP	60	60	993	492	372
L1AD277	AC006265.1	17	GTACAAACCATGGACCAGTT	ATGCAAGTATTTGGCATCTT	FP	55	60	6451	386	239
L1AD278	AL121757.7	UNK	INSERTED IN REPEATS		R					
L1AD279	AL157881.14	UNK	INSERTED IN REPEATS		R					

L1AD280	AC006131.1	UNK	INSERTED IN REPEATS		R					
L1AD281	AF036938.1	X	CAGAGTGAAGTGCTTGGTTT	CTTAATATTTGGGCCATGC	NR	60	55	1342	494	590
L1AD282	AL450303.10	1	NO RESULTS		NR					
L1AD283	AL358434.16	UNK	INSERTED IN REPEATS		R					
L1AD284	AL357141.8	6	NO RESULTS		NR					
L1AD285	AL359252.17	6	ATCCAATCACCATCATCAGT	ACCTGTGTTCCTATCTTTGC	FP	55	55	823	423	272
L1AD286	AL354937.12	9	TTTAACAACGCACACTTAGC	ATTAAGCAATGGCAGGAAT	FP	60	60	1385	337	444
L1AD287	AL356430.19	13	TTGAAATCAATAATGAGGGATA	AACATCAGTCAGCTAAAGCA	FP	55	55	518	277	256
L1AD288	AL121574.19	UNK	INSERTED IN REPEATS		R					
L1AD289	AL390039.10	UNK	INSERTED IN REPEATS		R					
L1AD290	AL158167.15	10	CCATGCCTCAACATCTCA	ACCTTCCTTATCTTCCCTTG	IF	60	60	750	175	237
L1AD291	AL157398.6	10	TGGAAAAATATCCCATAATGA	TTTCAGATGGTTTTTCAACA	FP	55	55	6277	180	311
L1AD292	AL136970.8	6	GGCAAATTGAGTCAAAGATG	AACTCATTCACAGTAGCAACAA	FP	60	60	6281	206	200
L1AD293	AL136117.12	6	TGGGAATCAGGAAATTTAAC	CCTATTTCTTGGGTTTTCTG	FP	60	60	2300	199	429
L1AD294	AL356286.8	X	INSERTED IN REPEATS		R					
L1AD295	AL158201.19	X	AAAGAAAGAAAACACCCACA	CTCACGTATTATTCCGATTTG	NP		60	2579	245	699
L1AD296	AL136441.16	13	AACCAAGGACTTACACATGC	ACTACCACTCATCCAGCAAA	FP	60	60	6518	461	261
L1AD297	AL357499.10	UNK	INSERTED IN REPEATS		R					
L1AD298	AL136455.6	1	TGCCACATCTGTTCAGTAAA	GAAATAGGCTCGTTTTCTCT	FP	60	60	1906	399	351
L1AD299	AL359502.14	13	TTAATGCAAGCAGAGTTTCC	TAAGAACCCATGGTCCAGTA	FP	60	55	6269	180	291
L1AD301	AL139334.10	6	AGTTGTCTGAGGAAACACCA	TACGCAGCATCAAGTAAAGA	FP	60	60	1823	700	288
L1AD303	AL139092.12	6	INSERTED IN REPEATS		R					
L1AD304	AC005358.1	17	ATCAGTGGTTCTTTGTCCTG	AGCAGTTCACAGTCCTTAGC	FP	55	55	1230	226	248
L1AD305	AC004768.1	5	GCCAGGAGATAATTTGTAGC	TACCTTGCCAGTAACCTTCT	FP	60	60	2726	386	330
L1AD306	AC004389.1	X	END OF CONTIG		EC					
L1AD307	AC004074.1	X	INSERTED IN REPEATS		R					
L1AD308	AC004523.1	UNK	INSERTED IN REPEATS		R					
L1AD309	AL138702.8	13	GCATTGCAGAAGAAAGCTA	TACCTCCAAGGCAAAACTTA	FP	60	60	1547	273	293
L1AD310	AL121946.20	6	CAACACACGTACAGGTATGC	TTAGCCTCTGTCTTTTGTGC	IF	60	55	6557	519	372
L1AD311	AL135932.7	11	TGACCTGTTCTGATGATTGA	CTTCTCAGGGTATCTGTCCA	FP	55	55	2281	271	327
L1AD312	AL136086.8	1	TTGGGGATAACTTTAACTGC	CCTTTTCATCCTCATGTTTT	IF	55	60	6284	228	209
L1AD313	AL137026.21	10	GCAGGAGAGAGTAAAGGGTTA	TGACAACCACTGCTATCAAG	FP	60	60	1382	86	165
L1AD314	AL121938.10	6	GGCTCAGGGAGATTTGATA	TCTGTTGTACTCTTTCAGGAACT	FP	60	55	3462	311	322
L1AD315	AL121933.15	6	GGTAACTAAAGCCATTGCAG	TATCTTTGGATGCTGCATAA	FP	55	55	2636	429	316

L1AD316	AL133547.16	9	INSERTED IN REPEATS		R					
L1AD317	AL157378.8	6	INSERTED IN REPEATS		R					
L1AD318	AL355871.5	1	TGTGGCTAATTCTGAGACCT	ACATGAGTTATCGTGGCATC	IF	60	60	631	176	175
L1AD319	AL157361.6	13	CCCAATGAACCTGTTGTAGT	GGATTTACATGCCACTTAGG	FP	55	60	392	188	241
L1AD320	AL157360.8	UNK	TCCAATGTTCTCTTAGAGGAGT	TCAACATGCAAAAGACTGAA	FP	60	55	489	114	248
L1AD321	AL139115.5	9	CTTGTCCATTTTCTCCACTG	CAACCCAGTAACTCCACTTC	FP	60	60	1193	80	200
L1AD322	AL049796.28	1	TTCTTCCTGGAAAATTGCTA	TTCCTATGAATCCAGTAGTGC	FP	55	60	6512	434	251
L1AD323	AL117345.21	6	GATGGCTTCAAATCCTTCTT	CACTTCAGATAGAACAAGAGCA	FP	60	55	3744	395	379
L1AD324	AL109920.15	6	TATCATTCCTTCAGGCCATA	GGTGAATGCTTTGGACTTTA	FP	55	60	1568	249	280
L1AD325	Z98950.1	X	TCGGCAGCACATATACTAAA	TCCATAGCCAAGTGAGTTTT	FP	60	55	1001	207	283
L1AD326	AL050309.4	X	INSERTED IN REPEATS		R					
L1AD327	AL030998.1	X	AAAACATATTTGGAGGAGCA	GTGACCTGGTGTTTTTGTCT	FP	55	55	6315	202	314
L1AD328	AL133353.6	10	TGCTAATAAAAGCACTCTGAAA	AAGATGGTGAATGTTGTAGGA	FP	55	60	2610	155	284
L1AD329	AL136169.6	UNK	INSERTED IN REPEATS		R					
L1AD330	AL133404.8	6	INSERTED IN REPEATS		R					
L1AD331	AL136363.4	X	ATTTCTTCTGCAGCTCTGAC	CATGATAACTTTGGTTTGTCAC	FP	60	60	6213	188	279
L1AD332	AL133247.1	2	TGACTGACCACTGTATGGAA	GTGGCTGTTTGGATTCTTTA	FP	60	60	1399	204	247
L1AD333	AL078604.10	6	INSERTED IN REPEATS		R					
L1AD334	AL021877.1	22	TTGACTTGTTTAGAAAGGGATT	GGATAAAGCTGAAAGCTCAA	FP	55	60	6322	233	215
L1AD335	Z70758.1	X	TCATCCAGCATTGAATCAG	TTGGTAGAAAGTGAAGTGGAG	FP	60	60	571	199	238
L1AD336	AL096706.10	UNK	INSERTED IN REPEATS		R					
L1AD337	AL049589.15	X	INSERTED IN REPEATS		R					
L1AD338	AL021069.1	1	AAGAATCCAATTTGCAACAG	TTTGATTCGGATTACACTGA	FP	60	60	6248	173	233
L1AD339	Z97181.1	X	GTTAAAATGCCAGGCTGAT	TGAGAAATGTGTTCTCCAAA	FP	55	55	1169	136	349
L1AD340	AL031117.1	X	INSERTED IN REPEATS		R					
L1AD341	AL034348.5	6	TGACTTCCATTTCAGGTACTC	CCACATTAGAGGTTTTCCAA	FP	55	60	4229	143	293
L1AD342	AL022399.2	1	TATGCATTTCCATGACTTGA	GTGGTAGGAGTAGGGGAAAG	FP	60	60	6795	342	708
L1AD343	AL033530.1	1	INSERTED IN REPEATS		R					
L1AD344	AL031313.1	X	INSERTED IN REPEATS		R					
L1AD345	AL023806.1	6	AGTACCAATGAAGTGCCATT	CAGGAGCATAAATAGGACCA	FP	60	60	1770	379	500
L1AD346	Z80232.1	X	CGGAAAATCCTCAGTCATC	ATGCCACAGCTTAAAAGTTC	FP	60	60	1065	261	309
L1AD347	Z84720.1	X	INSERTED IN REPEATS		R					
L1AD348	Z93018.1	X	NO RESULTS		NR					
L1AD349	Z99128.1	6	AGCACTCCTTTTATGAAGTCAACC	AGAGGAGAGAGTGGTTGATATTGG	FP	55	55	2851	1223	565

L1AD350	Z82170.1	UNK	GGCAGACCAAATGGATTAT	GATCCAAATATCAGACAAAATGT	FP	55	60	6342	288	184
L1AD351	Z95126.1	X	TGACATGCTTCCCTAAGTTT	TATAGAAAGTGAGGCCCAGA	FP	60	60	537	363	313
L1AD352	Z95325.2	X	CTTGCTGAATTAATCCCTTT	GGAAGAAATGATCCATAAGAAA	FP	55	55	3497	355	346
L1AD353	AL022308.1	X	CAAGGGGAAATCTCACAATA	GGACTTTGGGACTTACATCA	PARALOG	55	60	6238	174	263
L1AD354	AL023095.1	X	TCATCTTGCTCCCAAATATC	TCCTTAACACAGTCAAGTGAAC	FP	60	60	4839	170	338
L1AD355	Z98948.1	X	NO RESULTS		NR					
L1AD356	AC000111.1	7	TGTGGCTATGTGAGATGAGA	CCTTAATTTGAGGGGTTTTT	FP	55	55	4633	326	385
L1AD357	AP004241.2	11	CATAGGACGTTCAAGTGTGA	ATTGTCTATGGCTGCTTTCT	FP	60	55	765	387	593
L1AD358	AP002803.3	11	AGGTTTTGAGGTTTGCTGTA	TCCCAATAATCACTTTCCAC	FP	55	55	6274	205	264
L1AD359	AP002002.4	11	AAGGGCATATAAAACTGGTG	GCACCCATTAACTCATCATT	FP	55	60	6460	356	328
L1AD360	AP000764.4	11	CCATGCTTTCCACTCTTTAT	GCAGAAAAGGGTGTTCATA	FP	60	60	379	179	240
L1AD361	AP002784.3	11	GGAAAAATGACAGTCAGGAG	GCCTACCCAATGAATATCCT	HF	60	60	1031	149	258
L1AD362	AP003719.3	11	INSERTED IN REPEATS		R					
L1AD363	AP000811.4	11	CCATTACTTGAAGCAGAACC	CTGTGGGTCTCAGATCATTT	FP	55	55	6419	367	175
L1AD364	AP001977.4	11	TAAACTGGGGCTAGAAGTCA	CCAATTGAGAACCATCTTGT	FP	55	55	6335	383	344
L1AD365	AP002982.2	8	ACAGAGATTTCCTGGGCACT	TCAAACTGCATGCAAAATCC	FP	55	55	811	109	208
L1AD367	AP000789.4	11	CCAACAGGGATCAAAGGTTC	GCCACCTTGAGTTGGTGAAG	FP	55	55	378	147	175
L1AD368	AP002006.5	11	TTTCTTTTCCTACTCTCCCTCTC	GAGAAATAAAGGCAATTGCTCAC	NP		55	4593	186	922
L1AD369	AP001485.4	11	AAAACATATAAGCGGCCAAC	CAGCACCTGTTATGGTTTGA	FP	60	55	2437	466	187
L1AD370	AP000462.2	11	TAAGAAGAGGGGAGGAGACT	GCCTCTATGAAGCAGGTATG	FP	55	60	793	178	237
L1AD371	AP001709.1	21	CTAAATTGCTCCATTCCTTG	ATCACTGTAGGGTGATCCAG	HF	55	55	2525	581	562
L1AD372	AP001678.1	21	CTTACGCCTCAATTATCTGG	TGCAATTGATCTTACAAGGA	FP	55	55	2325	280	269
L1AD373	AP001674.1	21	CAAATAGCCAGCACAATATG	TTGTCATTGGTCTTTTGTCA	FP	55	60	823	165	226
L1AD374	AP001669.1	21	INSERTED IN REPEATS		R					
L1AD375	AB009801.1	14	AATCCACCTGCAGACATTAC	AGAACATCCCCTATCCAAAC	FP	55	55	688	87	202
L1AD382	Z95325.2	X	INSERTED IN REPEATS		R					
L1AD383	AC090791.6	11	TGGTGGTCTCAGAGTAAACA	ACCCAAAACATCATTAGTGC	FP	60	60	1642	117	1026
L1AD384	AL136441.16	13	INSERTED IN REPEATS		R					
L1AD385	AP003123.2	11	GCACAGGTTTATCTCCTTGA	ATTGAAGACCTGCAATTTGT	FP	55	55	6379	284	287
L1AD386	AC114975.2	5	INSERTED IN REPEATS		R					
L1ADY8	AC010970.3	Y	TCACACGTATCCCTTTGCAG	TTTTCTGTGAAACATCTTGGAGA	FP	55	55	1813	115	204

* Indicates L1 preTa element identified by Ovchinnikov 2002 (Reference #28)

1. Chromosomal location was determined from Accession information or by PCR analysis of NIGMS monochromosomal hybrid cell line DNA samples. L1 elements with unknown locations are denoted UNK.
2. Elements at the end of sequencing contigs are denoted (EC), those residing in other repeats (R), those having paralogs (PARALOG), and elements with inconclusive PCR results (NR). Elements represented here are classified according to allele frequency as: high frequency (HF), intermediate (IF), No pre-integration site in primate samples tested (NP), or as fixed present (FP) insertions. Fixed present: every individual tested had the LINE element in both chromosomes. Intermediate frequency insertion polymorphism: the element present in more than 30% of alleles tested and no more than 70% of the alleles. High frequency insertion polymorphism: the element is present in more than 70% but not all alleles tested. Indeterminable data is denoted (-).
3. Amplification of each locus required 2:30 min @ 94°C initial denaturing, and 32 cycles for 1 min 94°C, 1 min Annealing Temperature (A.T.), and 1 min elongation at 72°C. A final extension time of
10 min at 72°C was also used.
4. PCR product sizes: Empty product size is calculated computationally by removing the L1 preTa elements and 1 direct repeat from identified filled site. Subfamily specific product size is calculated from internal subfamily specific primer located in the 3' UTR to the proximal 3' primer. In cases where target site duplication sequence were not found flanking the element PCR product sizes may vary from those reported.

Table 2. Autosomal preTa L1 allele frequency and heterozyosity.

	African American					Asian					European					South American					
	Genotypes					Genotypes					Genotypes					Genotypes					Avg
Element	+/+	+/-	-/-	f^a	Het[b]	+/+	+/-	-/-	f^a	Het[b]	+/+	+/-	-/-	f^a	Het[b]	+/+	+/-	-/-	f^a	Het[b]	Het[c]
L1AD10	0	5	14	0.13	0.23	0	8	12	0.20	0.33	3	7	7	0.38	0.49	3	7	10	0.33	0.45	0.37
L1AD14	9	10	1	0.70	0.43	4	8	7	0.42	0.50	16	4	0	0.90	0.18	17	2	1	0.90	0.18	0.33
L1AD19	13	7	0	0.83	0.30	15	2	0	0.94	0.11	14	6	0	0.85	0.26	14	6	0	0.85	0.26	0.23
L1AD20	18	2	0	0.95	0.10	19	1	0	0.98	0.05	16	0	0	1.00	0.00	19	0	0	1.00	0.00	0.04
L1AD75	0	5	15	0.13	0.22	0	1	18	0.03	0.05	1	9	9	0.29	0.42	0	9	11	0.23	0.36	0.26
L1AD77	1	5	11	0.21	0.34	0	1	19	0.03	0.05	0	3	13	0.09	0.18	0	6	12	0.17	0.29	0.21
L1AD82	19	1	0	0.98	0.05	17	0	0	1.00	0.00	20	0	0	1.00	0.00	19	1	0	0.98	0.05	0.03
L1AD96	13	5	2	0.78	0.36	15	1	0	0.97	0.06	5	10	5	0.50	0.51	11	7	2	0.73	0.41	0.34
L1AD100	19	0	0	1.00	0.00	19	0	1	0.95	0.10	20	0	0	1.00	0.00	20	0	0	1.00	0.00	0.02
L1AD101	16	4	0	0.90	0.18	10	5	0	0.83	0.29	13	6	1	0.80	0.33	11	9	2	0.70	0.43	0.31
L1AD102	14	0	0	1.00	0.00	14	1	0	0.97	0.07	12	1	2	0.83	0.29	0	4	16	0.10	0.18	0.13

L1AD125	12	7	1	0.78	0.36	14	6	0	0.85	0.26	20	0	0	1.00	0.00	19	1	0	0.98	0.05	0.17
L1AD135	19	1	0	0.98	0.05	20	0	0	1.00	0.00	20	0	0	1.00	0.00	20	0	0	1.00	0.00	0.01
L1AD160	11	5	4	0.68	0.45	5	11	4	0.53	0.51	4	12	1	0.59	0.50	4	8	3	0.53	0.51	0.49
L1AD176	7	3	2	0.71	0.43	2	9	5	0.41	0.50	0	1	15	0.03	0.06	1	0	11	0.08	0.16	0.29
L1AD186	4	7	8	0.39	0.49	14	5	1	0.83	0.30	5	10	2	0.59	0.50	4	11	5	0.48	0.51	0.45
L1AD189	14	5	0	0.87	0.23	19	0	0	1.00	0.00	20	0	0	1.00	0.00	19	1	0	0.98	0.05	0.07
L1AD208	14	6	0	0.85	0.26	19	0	0	1.00	0.00	14	0	0	1.00	0.00	14	0	0	1.00	0.00	0.07
L1AD213	7	9	3	0.61	0.49	2	12	5	0.42	0.50	2	2	5	0.33	0.47	8	5	7	0.53	0.51	0.49
L1AD219	3	14	3	0.50	0.51	0	10	10	0.25	0.38	1	5	14	0.18	0.30	2	11	7	0.38	0.48	0.42
L1AD230	14	6	0	0.85	0.26	19	0	0	1.00	0.00	20	0	0	1.00	0.00	20	0	0	1.00	0.00	0.07
L1AD232	13	7	0	0.83	0.30	8	7	3	0.64	0.47	12	2	0	0.93	0.14	13	4	1	0.83	0.29	0.30
L1AD240	13	3	0	0.91	0.18	20	0	0	1.00	0.00	13	0	0	1.00	0.00	20	0	0	1.00	0.00	0.04
L1AD251	3	9	7	0.39	0.49	10	8	2	0.70	0.43	14	4	0	0.89	0.20	8	11	1	0.68	0.45	0.39
L1AD253	11	6	3	0.70	0.43	0	14	5	0.37	0.48	4	8	7	0.42	0.50	0	6	14	0.15	0.26	0.42
L1AD255	1	8	10	0.26	0.40	1	9	10	0.28	0.41	6	7	7	0.48	0.51	3	14	3	0.50	0.51	0.46
L1AD264	4	10	6	0.45	0.51	2	9	8	0.34	0.46	2	7	7	0.34	0.47	3	11	6	0.43	0.50	0.48
L1AD290	7	12	1	0.65	0.47	4	8	7	0.42	0.50	3	13	0	0.59	0.50	6	9	5	0.53	0.51	0.49
L1AD310	5	6	7	0.44	0.51	0	5	15	0.13	0.22	5	2	5	0.50	0.52	6	5	7	0.47	0.51	0.44
L1AD312	0	4	16	0.10	0.18	11	6	2	0.74	0.40	2	9	5	0.41	0.50	2	7	9	0.31	0.44	0.38
L1AD318	4	12	4	0.50	0.51	2	12	6	0.40	0.49	4	8	8	0.40	0.49	3	11	6	0.43	0.50	0.50
L1AD361	17	3	0	0.93	0.14	19	0	0	1.00	0.00	20	0	0	1.00	0.00	20	0	0	1.00	0.00	0.04
L1AD371	15	5	0	0.88	0.22	18	2	0	0.95	0.10	20	0	0	1.00	0.00	20	0	0	1.00	0.00	0.08

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a. f represents the frequency of the element

b. This is unbiased heterozygosity.

c. Average heterozygosity is the average heterozygosity for all populations

Table 3 – Ya-lineage PCR Primers, Chromosomal Locations and PCR Product Sizes.

Name	Accession	5' Primer sequences (5'-3')	3' Primer sequences (5'-3')	A.T.[1]	Human Diversity[2]	Product Sizes[3] Filled	Empty	Direct Repeat
CHROMOSOME 1								
Ya5NBC14	AL050342	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	-
Ya5NBC19	AL109948	AATCACTGTTACTCATGGGGTATCT	AGACCTACGTGCCTTACTCACTGT	60	FP	433	116	CCTTTTTGATATTTTC
Ya5NBC44	AL096840	CATTCTCTCCTTTGGTCCTCTTTAT	GTGAGTTTGGGGATATGGTGAG	55	FP	525	202	CTCTATGTCACTTCTT
Ya5NBC47	AC007227	CTCAAGATTGGCCTATAGTCGTTAT	AGACACAGGTATCCAGTGAAAGAGT	55	FP	526	200	AAGACTGCTTTTAT
Ya5NBC50	AL096829	NOT AMPLIFIABLE	NOT AMPLIFIABLE	-	NA	-	-	NONE
Ya5NBC83	AL022101	AGGGAAGTCAGGCAGAAC	CCTTCCCTAGGAGCACAT	55	FP	384	106	CAGGAGGATCTTCTT
Ya5NBC91	AL034378	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	NONE
Ya5NBC124	AL022310	CTAGACAGTGCAACAGTTCCTAAATACAG	CATAATGGAAAACTCCATGTGCTAC	60	FP	457	131	AAAACATAAACCC
Ya5NBC149	AL033525	GTGTTACTGTGGCCAACTATCTCAT	ACTTATATGAGCGGGGTACAGTTCT	60	FP	466	155	ATGTTTAATAAG
Ya5NBC166	AC004040	CCCTTGGCTCTATAGATAAAGTTGG	ACTGCACCAAAACTAGAGAGGAAA	60	FP	532	210	CAAAATTGACATCTT
Ya5NBC168	Z97876	AGTGCTAACCAGAGATGTGTGTGAC	TTAGTGGAATGTTCCAGGACTGTAT	45	FP	492	164	NONE
Ya5NBC213	AL078463	INSERTED IN REPEATS	INSERTED IN REPEATS	R	R	-	-	AAAACAAAACTGGC
Ya5NBC307	AL133289	TCCCTGAAACAAAACCCATT	AAGACCACAACCCCCATACA	65	FP	450	144	CTATAATT
Ya5NBC332	AL050342	TGGAAACAGAGCAATGGACA	ACACAGGTCCTTGAATATGAGC	65	FP	631	416	ATACAAAAAATTAGC
Ya5NBC346	AL096776	NOT AMPLIFIABLE	NOT AMPLIFIABLE	-	NA	-	-	AGGGCTGTTTTTT
Ya5NBC347	AL035411	CATGCCCATTGCTTTACGTT	TGGGGTAGATGGACTCATCC	60	IF	465	140	ATCATTTGAATTATCTTT
Ya5 442	AL031275	NOT AMPLIFIABLE	NOT AMPLIFIABLE	-	NA	-	-	GAGATGGGG
Ya5 471	U67233	GGAGGGGGATTTGAGGTCT	CCACTTGCAGAGATTGGTGA	60	FP	106	453	GAAAAGGACTCCTGCA
Ya5 553	AL136147	GGACTTTTGCCCCAATTTTT	TTCCCACCTGTCCTGTTCTC	60	FP	162	480	AAAAGTCCCAGCCCA
Ya5 559	AL390023	TCAGCATCAAAAAGACCTTGG	CAATGACCCTGCAAGGTAGG	60	FP	130	458	GAAAAATGGGAATAATAA
Ya5 561	AL157837	TGGTTGATGGGAGATAGTGG	CCAATGGGAGGAAATTGTGT	60	FP	150	487	AAAAACTTGAGACATG
Ya5 562	AL135926	TGGATGATAACATGGCTGCT	AGGAGGTGAGTTTTTCCTTCA	60	FP	88	408	GCTAGCTTTTTCTTT
Ya5 566	AL078645	CAGCATGTCACTGAGCTGAA	ATGACAGGGGTCCCGTAATA	60	FP	130	452	AGAAAAGGTACGGTAA
Ya5JW574	AL136372	GGTTTCACCATTGCTCAGTAGAT	GAAGAATTTGGGGTGGTACACTA	60	FP	107	396	ATCAATACTTC
Ya5ACA585	AL031428	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	NONE
Ya5ACA586	AL512665	CAAAAGGGCTTGATGTTTGG	GGCTCTCTGCATCTCTGTCA	60	FP	123	439	AATAATA
Ya5ACA587	AL162595	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	GATATACAAATAGG
Ya5ACA588	AL359510	ATTTCGCAAGGATGCCTTTT	TGGGGAGAACTGATGTCTTTG	60	FP	188	500	AAGAGGGATGT
Ya5ACA589	AL354721	CATTGCTTGAGCATGTGTCC	TGAAGCTTGGAGCCCAAATA	60	IF	141	464	TAAGCGAGAGAC

(table cont.)

Ya5ACA590	AL445669	ATCACAGGCCGATACAGTCC	TTTGTTTATAAGCCCACAAGTAACA	55	FP	160	469	AAAAGAAAATAGTATT
Ya5ACA591	AL359185	TCTTCAATTACTGCTTCTGTTCCA	GCAGAACTAAAATATGCATTTGG	60	FP	163	475	AAAACAATAC
Ya5ACA592	AL391994	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AAAAAGCCATTTCC
Ya5ACA593	AL109810	CAGAGCCTTAAGACGTGAGAGTT	GGAAAGCTCAGAAAAGACAGGA	60	HF	195	500	AAGACCAGCCTGGC
Ya5ACA594	AL118511	TTGGGAGATGAGATCACG	GACAGAGTCTCATTCTGTTGC	60	FP	375	693	AAAAAAAAAAAAGAC
Ya5ACA595	AL512271	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AAAAATCAGCC
Ya5ACA596	AL357055	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AAAGGGGAGTTC
Ya5ACA597	AL358215	GCAGGTGACAATGTCCGTAA	TCCATCAACTCTCCCTGCTC	60	FP	143	491	AACACCTTTAA
Ya5ACA598	AL356583	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AAAGACTGTCCTGGG
Ya5ACA599	AL390036	CCTGTGACAATCAAACAGCAA	GCACTCCACATCTGTAGCTCTC	55	FP	156	486	AAAAAGTGTTCATTTTG
Ya5ACA600	AL122008	TGTTTAGGACAAAGCAAAGG	CCATGCTTCTTGTATATCCTG	55	FP	165	476	AAAAGAAGTTCCTT
Ya5ACA602	AL591292	TCGATAAAATTGCTCCTGTGG	GGTCAGTTTCCTGTCCCTCA	60	FP	167	460	AAAAAACTAACTTTAAA
Ya5ACA603	AL050342	GATATTTATCGAGCGAGTGC	CCAGGTTCACACCATTCT	60	FP	~130	501	NONE
Ya5ACA604	AL355274	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AAAGCCATGCC
Ya5ACA605	AL020995	NOT AMPLIFIABLE	NOT AMPLIFIABLE	-	NA	-	-	AAAAATTAG
Ya5ACA606	AL355274	TGGAACAGGCTTAGAACAAT	GGATTTTAAAGCACCCACT	60	FP	175	490	AAAAGTTAGTAGCT
Ya5ACA607	AL512665	NOT AMPLIFIABLE	NOT AMPLIFIABLE	-	NA	-	-	AAGAAATCAAGCCA
Ya5ACA608	AL513202	GTAGAGACACAAGGCACCCC	ATCTGTTGAGCCAAACCTGG	60	FP	169	484	AAAGAAACCACAG
Ya5ACA609	AL133517	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AAAAAATGATGAGTTC
Ya5ACA610	AL583808	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AAGAATGTTG
Ya5ACA611	AL596133	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AAAAAAAGTTGTT
Ya5ACA612	AC099677	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AAAAAAATAGG
Ya5ACA613	AL109618	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	CTAAACA
Ya5ACA614	AL512307	TGGTGCTTCTTGCTATACCATC	CAAACATTTTCAGGCTGGATT	60	LF	166	481	AAGATACTTTGATTAG
Ya5ACA615	AC105276	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AAATC
Ya5ACA616	AC093424	CAGCGTCCCCTTCTTCTTATT	GGCACACTGGTCCAGGTACTA	60	FP	181	500	AAAAAGTAGTTATT
Ya5ACA617	AL133286	TTTTAGCACAAAGGAACGGC	CTTCTGCAGAGAGGGTGGAC	55	FP	482	791	AAAAAATTAGCTGGGC
Ya5ACA618	AL035411	GCTACCCTCCTATGAGTGACAGA	CATGCCCATTGCTTTACGTT	55	HF	104	447	TTCAAATGAT
Ya5ACA619	AL445193	NOT AMPLIFIABLE	NOT AMPLIFIABLE	-	NA	-	-	AGAGAGATCAG
Ya5ACA620	AL133289	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AAGAGGACGA
Ya5ACA621	AC114489	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AAAAAAAGAAGA
Ya5ACA622	AL160171	TGCACATGTGTCTCCAACAA	GCCCGTACAAAGACAGAAGC	60	FP	116	430	AAGAAACCCTG
Ya5ACA623	AL138847	GAAGTTGATGGACCACGTCA	GGGCCCACAGCTCTTTTAT	60	FP	140	482	GATTATAAAAGAG
Ya5ACA625	AC099791	CAAACCTTACTCATAGGCTCCC	GTGTCCTTAAGCTTTTAAATGTAGC	60	FP	101	413	GATTGCTA

(table cont.)

Ya5ACA626	AL356986	TCACTAAACCTCCCTGCCTC	CTCCTGCCACTGAACAGACA	60	FP	125	436	AAAATTCTAGAAAAT
Ya5ACA627	AL592285	AGCAGGGAATAGAAAACCACA	GTCTTTCTGGGCTGCATTCT	60	FP	198	499	AAAAAAAAATTAGC
Ya5ACA628	AC097063	NOT AMPLIFIABLE	NOT AMPLIFIABLE	-	NA	-	-	NONE
Ya5ACA629	AL592285	CCAGTGGAAGCTGGATTTTC	TCAATAGTCAGTGAGCACCACA	55	FP	179	501	AGAAATGCTTTTAG
Ya5ACA630	AC093426	CCAGTCTGCTAAGACAGTTTTGAA	AGCGGGTACAGTAGGCAGAA	55	LF	159	498	AAGAAGGAATTGG
Ya5ACA631	AL359258	TCCCTGCTCTCTTGTTTTCC	TCGAATGCTGTGTACAAAAGAC	60	FP	60	401	AAAAGTAAGAAGAGTC
Ya5ACA632	AL358854	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AAAAATTAGCTGGAA
Ya5ACA633	AL365362	AATCCATGTAACGGCATGGT	CCCTCAGTTCTCATCTAACCTTGT	60	FP	172	487	AAGAATAGCACATA
Ya5ACA634	AL391239	NOT AMPLIFIABLE	NOT AMPLIFIABLE	-	NA	-	-	NONE
Ya5ACA635	AL109660	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AAAACTTTTGTTAGG
Ya5ACA636	AL357137	ACTTAAAGTGTTCAGCGGGG	ATTTTCCACCAACCAGGACA	60	HF	139	442	AAAGTGTTCAGCGGGG
Ya5ACA637	AL357912	AAATGCCCCCTACAAAGACA	TGTGTGTCCCTGCATCTCTC	60	IF	170	484	AAGAATTTTAAG
Ya5ACA638	AL512271	GGGCTTTGAAAGTCAGGAGA	AGCCAATTATCCCAGTGCAA	60	FP	130	469	GAAAGTCAGGAGA
Ya5ACA639	AL591742	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AAATACCCAGGGTTCG
Ya5ACA640	AL031294	CAACCACCTCACCTCTTTCAA	TGTGTCACAGTGTTTGGCAAT	60	FP	125	451	AACAAATATTCA
Ya5ACA641	AC093433	CCAACTCCAGGCTTCTTTCA	TTGTTCTCCTTTGCCCATTT	60	LF	151	471	AGAAAAATGGGCA
Ya5ACA642	AC135803	NOT AMPLIFIABLE	NOT AMPLIFIABLE	-	NA	-	-	AGAAAGAC
Ya5ACA643	AL445648	TGGGTCTAGCCAATCATTCA	CCCAATCCTGCAGAGGTCTA	60	FP	150	468	AAGATTAGCCATAGCC
Ya5ACA644	AC095036	TTGCTTAGAAAATCATGAGAGAGAA	AGGGATGGTCACATGATGAAG	60	FP	164	485	NONE
Ya5ACA645	AC093118	TGAGCAGGAACTTTGCATTC	CAGATCAGTTCTTCACGGGAG	60	IF	183	500	CTAGTGTATCAC
Ya5ACA647	AL358533	ACGTAAGCCTCAAAAAGGCA	GGCACTGCAGATACAGTGTGA	60	HF	58	375	AAAATCCTTTTAG
Ya5ACA648	AC093425	NOT AMPLIFIABLE	NOT AMPLIFIABLE	-	NA	-	-	AAAAGAACTCCATTTTAG
Ya5ACA649	AL122000	NOT AMPLIFIABLE	NOT AMPLIFIABLE	-	NA	-	-	GAATTAAACTCTG
Ya5ACA650	AL035705	NOT AMPLIFIABLE	NOT AMPLIFIABLE	-	NA	-	-	AGAAAATAGAAGGCCCAG
Ya5ACA651	AL513480	GACCACCAAGATGTACCAGTGA	CTTAAGGATTGCAGATGGGG	60	FP	172	485	AAGATTTGTG
Ya5ACA652	AL157906	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AAAAGTATGCAGC
Ya5ACA653	AL359762	TGTGAAAATGCAGGAACACAT	ATTAAATGGCCTTCAATGCG	60	FP	712	1021	NONE
Ya5ACA654	AL359954	NOT AMPLIFIABLE	NOT AMPLIFIABLE	-	NA	-	-	AAGAGTGGACATCC
Ya5ACA655	AC093565	NOT AMPLIFIABLE	NOT AMPLIFIABLE	-	NN	-	-	AGAAAGTGCAGGTTTAG
Ya5ACA656	AC006031	TGCTCTGTGAGTGTTTTGCC	AAACATAGTCTTAAATTGCTGGGT	60	FP	166	481	AAAAAATTGTCTTTCTG
Ya5ACA657	AL391497	TCTGGCAGAAAGGTCAAGACT	CCTTGGATGAATTCCCAGAA	55	FP	128	449	AAAAGGAAAAAGA
Ya5ACA658	AC105276	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	NONE
Ya5ACA659	AC093578	TCTGTGCAAAGCAGAGGGAT	AACAATGCCTAGCACAGGGT	60	LF	163	478	GAAACCTCTGATTTG
Ya5ACA661	AC104838	ATCATCCTCCTACATGGCCC	TTGGGTTCTAATCCTGGGAA	60	FP	131	449	AAGATCCTTAATT

(table cont.)

Ya5ACA662	AC119749	CCTGCTGCTTCTGTGTTTCA	TTGCCATTTTCACTGACTGC	60	HF	176	499	AAAGAGTTCTTAGGGA
Ya5ACA663	AC073220	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AAGAAACTCACTC
Ya5ACA664	AL627095	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AAAAAGCTCCAGCACAG
Ya5ACA665	AC104332	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AAGAAATTGG
Ya5ACA666	AC095034	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AAAGAGTCAAGACCC
Ya5ACA667	AC105276	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	TCAATG
Ya5ACA668	AL604048	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AAGAAGAGAGA
Ya5ACA669	AC096538	TCTCCCTTTCTTCCTGAGCC	GAAATTTCCATGGCATTCAT	60	FP	142	454	AAAAAGACAGATA
Ya5ACA670	AL603844	NOT AMPLIFIABLE	NOT AMPLIFIABLE	-	NA	-	-	AAAAGAAATGGTTTC
Ya5ACA671	AL627310	NOT AMPLIFIABLE	NOT AMPLIFIABLE	-	NA	-	-	TTACTG
Ya5ACA672	AL590082	CGTGTGAAAATGTTGTGCTG	TTGCTGTGTATCCACTCCCT	60	FP	134	411	AAAAAATTAGG
Ya5ACA673	AL590082	GAACTTTGGGGCATTTTCCT	GTCAAAACCCCAGAGGTTGA	60	FP	193	485	AAGAACCTTGA
Ya5ACA674	AL109926	TTCCCTTTTTCCCTGCTTCT	TGGTCATGTTCCATGCCTT	60	FP	138	455	AGAGATAAG
Ya5ACA675	AL627310	AAACCAGTACATTGACTTCACAGC	TGCAGGGTTTTCAAGTGTTG	60	FP	173	497	AAAAACTAATGAACA
Ya5ACA676	AL445928	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AAAAATGATC
Ya5ACA677	AC093150	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AAGACAAAGTTACA
Ya5ACA678	AC093150	TCACAGGATACAAATAGGCAAAGA	AAAGCAAAATACAACTCAAAAGCA	60	FP	168	486	AAGAAAGAAATTGA
Ya5ACA679	AL691486	CGGGAAGGTAAAATGAGGTG	AACCACCACCACCATTAGGA	55	FP	591	928	AGAAAAAGAAGAGT
Ya5ACA680	AL672014	ACTTGGACCTTGTCCCACAG	CCAAGATCACCTTCAGGCTC	60	FP	136	458	AAAAATGTAAGCATGA
Ya5ACA681	AL590783	NOT AMPLIFIABLE	NOT AMPLIFIABLE	-	NA	-	-	AAACCTCTCTGT
Ya5ACA682	AL592151	TTCACTACCAACTCCCTGGC	AGGCGTAGGTTTCCCTTGAT	60	FP	138	469	AAAACAAGGAGATC
Ya5ACA683	AC096540	NOT AMPLIFIABLE	NOT AMPLIFIABLE	-	NA	-	-	AAAAAATCTG
Ya5ACA684	AC093151	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AAGAACTTGCTTT
Ya5ACA685	AL645769	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AAAAACTTCC
Ya5ACA686	AC113935	TGGTTTCCGCTGTTGCTATT	TCCAAAGCACAATACAGGGA	55	FP	157	484	AAGATGTTTGCTGTC
Ya5ACA687	AL662889	GAGCCGTATTCTTATGATTCTTTCA	TCATGGTGATGAGAATAGCCA	60	FP	192	500	AAAAAATTATT
Ya5ACA688	AL355480	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AAAAAACATGCTCCAG
Ya5ACA689	AL354949	CTGGATGCCAAAGGATGAGT	CACGTTCTTCTCTTGCCCAT	60	FP	76	402	AATAATCATGGGC
Ya5ACA690	AC084239	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	CAAAGATGG
Ya5ACA691	AL391650	NOT AMPLIFIABLE	NOT AMPLIFIABLE	-	NA	-	-	GAGAAGGAAGA
Ya5ACA692	AL137856	TGCCTGAAGCAGATTAAAAACA	GGCCACCTTCCAAACTGTTA	55	FP	142	463	AAATTAGAGACTCCA
Ya5ACA693	AL591594	GCAGTCACAAAACATCCCCT	TCATGATGTTCCAGTTTATTTCA	60	FP	163	495	AAGATGAAATACA
Ya5ACA695	AC092391	NOT AMPLIFIABLE	NOT AMPLIFIABLE	-	NA	-	-	AAAAAATACACACAC
Ya5ACA696	AL109966	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AAAAAAATCAATGAA

(table cont.)

Ya5ACA697	AL391476	CGCAGGAAAATATGCAGCTA	CTCCTTGTTGATCTTGGGGA	55	FP	150	463	AAAAAAATTCATA
Ya5ACA698	AL078463	GGAATGGGTGAGGGATACAG	TGATAATCATCAGCTCAGGGC	60	FP	55	361	AAAACAAAA
Ya5ACA699	AL096829	TTCTCCCATTTTCTTTTTACTAGC	ACATATTCAGAATCATTTGGCA	60	FP	60	370	AAAGAAAATATCTA
Ya5ACA700	AL592284	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AAGAAATATTTA
Ya5ACA701	AL391904	TGCAATACCCATTGCAAACA	TTTCAATTGTAGCATTTAAACTCCC	60	FP	505	834	TCTGCCTGCCTTGGCC
Ya5ACA702	AL356292	AATGCAATGCAGCAAACATC	CAGTTGCAGAGGACTCCCAT	55	LF	224	558	GAATTCTCAATTAAT
Ya5ACA703	AL357493	AAACCAACCACTTCGTCAGG	CTTGGTTCCAAACTTTCCCA	60	FP	126	445	AACAAGCGCAA
Ya5ACA704	AL592424	TGAGCTCTGTGGTTCACCTG	GTTTTCATCTCCTGGGCAAA	60	FP	62	380	AGAGAATAGATACAAAT
Ya5ACA705	AC068971	NOT AMPLIFIABLE	NOT AMPLIFIABLE	-	NA	-	-	AAAGATGTTTAGTGG
Ya5ACA707	AL049715	TCTCTTCACCTATGAAGCAGGAC	CAGAGGTGGAGGGCATAGTT	60	IF	189	500	AAGTATT
Ya5ACA708	AL138795	AGTTTGATTGCCCGTCAGTT	AAAAGGATCCGTGTAAGGGG	55	FP	75	379	AAAATAC
Ya5ACA709	AL513523	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AAAATAAAAATAAAAA
Ya5ACA710	AL135842	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AAGAATTTTTGCATG
Ya5ACA711	AL162734	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	CTCAAAATA
Ya5ACA712	AL353807	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AAGAATCT
Ya5ACA713	AL353807	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AAAGAAATTATTGG
Ya5ACA714	AL139410	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	NONE
Ya5ACA715	AL356483	GGCACCAGAGAACACAAGGT	ACATGTTTGGGGGATGATTG	55	FP	147	435	AAAGACAGTCCT
Ya5ACA716	AL356867	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AAAGAAAGTATATGTA
Ya5ACA717	AL356501	GGGCTAGGGAATGAAAGGAG	ATGTCACAGCCCTTCCTCTG	60	FP	56	383	AAAACTGGCTGG
Ya5ACA718	AL606752	NOT AMPLIFIABLE	NOT AMPLIFIABLE	-	NA	-	-	AAAGTGTAG
Ya5ACA719	AL356104	TTCATTTTGATTTTTCAACCATGT	TCCTTGGTCTTAATCTGTTTTTATG	55	FP	162	563	AAATAAGCTTG
Ya5ACA720	AL513205	CCCAGAGGCATTGAACATCT	TCTCTGTCACATTCCCACCA	60	IF	161	483	GAAAAGTAGGGCAAGG
Ya5ACA721	AL391825	CACCTAAACAAAGGGGGTCA	ACTTGGTGGCCTAGAGTCCC	60	FP	197	497	AAAAGATGGAAAGTTC
Ya5ACA722	AL357132	TTCCATGACAGCAGAGACCA	CCGACACACATTTTTGACCA	60	FP	120	421	AGAAAGTGCCTGGCATA
Ya5ACA723	AL591806	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AAAACTACAGTGAAA
Ya5ACA724	AL445197	TTGCCAAATGCAGACACCTA	GGAGGATGAAGCCAATCAAA	55	FP	161	479	AAAAATGCCAAATG
Ya5ACA725	AL359699	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AAGAAAATGTGGC
Ya5ACA726	AL359541	GCAGGACAAAGGAATCCAGT	AGAAGAGCAGACCAAGTGGC	60	FP	159	476	AAGAGTCCAGAGCA
Ya5ACA727	AL513364	CCTTTTGTGCTGCAAAATACA	GGCTGTCTTTTCGCTTTCTTT	60	FP	46	359	AAAATACACTATA
Ya5ACA728	AL590408	ACACGAGTGCTTCTTCCCAC	CATTCCCAGAGATGTTGCCT	55	LF	149	469	AGAAAAAAAGGACAC
Ya5ACA729	AC099561	GTCATGCATCTTCATGCCAC	CAGGACTCTGGCAGGTGACT	55	FP	89	418	AAAGACCTGAATGAG
Ya5ACA730	Z97876	NOT AMPLIFIABLE	NOT AMPLIFIABLE	-	NA	-	-	ATCAACAA
Ya5ACA731	AL031733	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AAAAATAG

(table cont.)

Ya5ACA732	AL031275	CTCTAAAGCCCCACCCCTAC	GATGGCAATACAGGAAAGGAA	60	FP	672	983	AAGAGATGGGG
Ya5ACA733	AL031726	CCTTGATTGCCAACACTGAA	GAAATTGGAGATTTGGGGGT	60	IF	175	500	GAAACAGTTCACTTGC
Ya5ACA734	AL358115	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AACAGTAAAACTC
Ya5ACA735	AC099569	GGCAGAGAGAGTTCCCATCA	TATCCTGCCTACCATCTGCC	60	FP	154	496	AAAAAGCTGGCTTTCTG
Ya5ACA736	AL049762	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AAAAATTAGCCGGTCGT
Ya5ACA737	AL031274	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AAGAGTAACCTTTTTG
Ya5ACA738	AL031965	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AAAAATACTGATTATG
Ya5ACA739	BX284613	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AAAGAAAGAAAA
Ya5ACA740	AL356377	GTTTCCCATCTCTGCCGTAA	AAATGCCCTTACATTGCTGG	60	FP	654	969	AAAAAAGTGTTT
Ya5ACA741	AL022400	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	GAAATCCA
Ya5ACA742	AF223391	GCAACCTACACAAAAGTGCC	TCCATTCCCCTTCTTTTTCA	55	FP	180	500	AAATACAC
Ya5ACA743	AL590987	TGCATATTTAAAGGGCTGACG	GCTTTCTTGTTTGATTCATGG	60	FP	149	471	AAAATGTTTAT
Ya5ACA744	AF223391	AGCAACCTACACAAAAGTGCC	TCACCTGGTTTCTACCCACAG	60	FP	165	486	AAGAAAATACAC
Ya5ACA745	AC023275	AAGGTTTTGTTCCTGTCATAATGTT	TGGTCCTAGAAGAAATGCACAA	60	IF	169	491	AAGACTTGTTTT
Ya5ACA746	AC019187	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AAAAGTGGAGAATCTT
Ya5ACA747	AL133383	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AAGAGAAGTTTAGA
Ya5ACA748	AL391098	AGGTTTCTGACTCCTTCACGA	TTGCTCAAATTCAATTACATAAGG	60	FP	180	473	AAAAAACTTCA
Ya5ACA749	AL356288	AGATGCCGTGCATGTGATAC	GCTTGATTTACACAGGCTGGA	60	FP	93	411	AAAAATGGAGGAAATC
Ya5ACA750	AL391645	GCACTTTTAACCCACATTATGC	AAAATGTCAAACAACAAAGAAAAG	60	FP	181	499	AAAGTACTACATA
Ya5ACA751	AL592447	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AAAAAAGGATGAGTTC
Ya5ACA753	AL139136	CCAAAAAGACAAAAAGTTTCATTTC	AAGCACTATTAAACTGGTGGACG	60	FP	196	499	ATTCTTAT
Ya5ACA754	AL356953	GAAGGTTGCAATAGGAGAAAAAGA	GTGGACAGAGAAGCATGCAA	60	FP	175	498	AAAAAACATTATTTA
Ya5ACA755	AL356953	ACCCTGGTGGAAAATGATGA	TCCTGGGTTCAAGCGATTCT	60	FP	274	592	AAAAAATTAGCCAG
Ya5ACA756	AL592114	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	ATAAAAATTAG
Ya5ACA757	AL356953	NOT AMPLIFIABLE	NOT AMPLIFIABLE	-	NA	-	-	AAAAGAACAG
Ya5ACA758	AC092810	TCGAGTCTTTAAGAAAGAGTTTTGA	AATCCAGCTCTTTTCCCTCC	60	FP	85	393	AAGAAAGAGTTTTGA
Ya5ACA759	AL513263	CCCACAATAAACATGTGGCA	CAAGCAGCTTAAACCAGGCT	60	LF	101	421	AAAAGTTTCAGGATTTG
Ya5ACA760	AL354681	GGGCCCTTTTCTTCTCTGTC	GAGATGGGTAGAGGCAACCA	60	FP	116	439	AAAAGCCTCATCCT
Ya5ACA761	AC104465	TGTTTTCTGCACACCAGTCA	GGGAGTTCCCGACCCTATAA	60	FP	182	498	AAAAACAGTCAAGAC
Ya5ACA762	AC099793	TCATAAGCCCCTCTTTCAGC	GCCCAGGCTACAACCAGATA	60	FP	175	496	TCCGTTCT
Ya5ACA763	AC118553	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AACATTAGGTATATCT
Ya5ACA764	AC096636	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AAAAGTACATGTAA
Ya5ACA765	AC114963	NOT AMPLIFIABLE	NOT AMPLIFIABLE	-	NA	-	-	NONE
Ya5ACA766	AC096636	CCTAAACACTCCAACCAAGCA	CCTCCACCCTCTCTCAATCA	60	HF	172	493	AGAAAGAAGCTATA

(table cont.)

Ya5ACA767	AL445488	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AGAAGTGAGAGACC
Ya5ACA768	AL583826	NOT AMPLIFIABLE	NOT AMPLIFIABLE	-	NA	-	-	GGTATAGATGCTTGAG
Ya5ACA769	AC092015	CCTGTCATTGATGAGTTTGAGG	GCATTTAAAGACCGCAAAGG	60	LF	164	484	AAGAAACAAAGCTTTTG
Ya5ACA770	AL513305	AAAGCCCAGTCAAATTTCCA	TGCTCTCTTAGCACAGAACATGA	60	FP	127	456	AAAAAATTC
Ya5ACA771	AL592406	NOT AMPLIFIABLE	NOT AMPLIFIABLE	-	NA	-	-	AAAGAATGGCTTATT
Ya5ACA772	AL356108	GGTATGTGTGGTTACTTTCCCTT	CAAGAGTCTGGCCTTTCTGG	60	FP	184	497	AAAATGTTAAGCTGATG
Ya5ACA773	AL592483	NOT AMPLIFIABLE	NOT AMPLIFIABLE	-	NA	-	-	AAAAGTAGAAAAAGC
Ya5ACA774	AL591380	AGATTGAGTGACTGGGCCAT	CCAGAACCTTGGTGTGACCT	60	FP	158	467	AGAGATAGATTTA
Ya5ACA776	AL031432	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	TTTG
Ya5ACA969	AL035404	AGAAGCTAACGTATGGTGGA	GATTACAGGCATGAGTCACC	53	FP	80	370	AAAAGGTAGATTTTT
Ya5ACA970	AL360270	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AAGATAATGGCCTT
Ya5ACA971	AL390234	GACACAGTGGGGGAAAAAGA	GCCCTGAAAGGCAATAACAA	60	FP	175	457	AAGAGCAACTGA
Ya5ACA972	AC092813	TGCCTTTGTTGGCTGAATTA	TGCCGTCTAAATTCCTGACA	55	FP	130	432	AAAGTTGGC
Ya5ACA973	AL449143	ACCCCCAGGAAGATTGAGAG	GAAAGGGAGGGCAGAAAAAG	55	FP	206	484	AAAAATGTTA
Ya5ACA974	AL049825	GCCCAGTCTAAGACGTTTTGTT	TGCAGGCACCTCTTTCTTTT	60	IF	85	368	AAAAGAAAGAG
Ya5ACA975	AC104458	CCAGAGGCAGACCAACATTT	TAAAGCCAGAGGGAAAAGGC	60	IF	116	399	AAAAATCCC
Ya5ACA976	AL713866	TGCAAAAGTGCACAACAAAA	TAATTTTGGCCATGGAGCAT	60	FP	79	363	AATATATA
Ya5ACA977	AC093419	AAAACCACAGAACTGGAAAAGAA	TGTCATTGTCCCTTCAATTTGT	60	FP	198	487	AAAGAAATACAAATTG
CHROMOSOME 2								
Ya5NBC5	AC007363	TAGGATATTACTGTACAAAGCCGTAGATTT	GTTTTAAGCTAAGCGTTATTACAAAAGAGT	60	IF	163	476	ATATTTTTTCTTT
Ya5NBC12	AC009307	GGAGTCAAAGGTACTTACAACGTCT	CTCCCTGTCTTCCTAACGTAATTTT	60	FP	129	470	AAAAATTACCCAGAAG
Ya5NBC76	M96868	ACTCTTTAGTTTGTAAGATGGCAAG	GGTGGAGGGAAGTAGCAGAA	60	FP	417	735	NONE
Ya5NBC95	AC009962	ATTATAGTAATAAATCCTGGAATTGGACCT	GAAATGAATCTATGGGATATGTTT	60	FP	148	489	GAATTAATCACAACTTC
Ya5NBC101	AC006030	CTCACTGACACTTTTGGTCAGACT	ATTTACTGAGCACAATGCCTCATAC	55	FP	204	519	AATAATGGACATGC
Ya5NBC108	AC007092	CATATGAGTGCCTGACTTTTACTACTTCTC	CTAAATACAGGATGAAAGGACTGGT	60	FP	215	567	GCAATTTGTG
Ya5NBC115	AC009316	AGAACAAACTGCACATCGAGTATCT	ACCTTCAAATTTCTCCTTTGAGGAC	60	FP	240	574	AAAAAAAGCATTTTC
Ya5NBC140	AC007877	GCAGCCCCAAGTGTTAAATTACTAT	GGTTGTGGTAATGTCATCATAAACG	60	FP	135	471	GATTATTAGCTTTT
Ya5NBC142	AC007392	ACATTCTAGGACACCTGTCAGTCAT	GGTCAATAGCATGGGAAAGAATATC	60	FP	321	663	AAGAATACAACCTTT
Ya5NBC301	AC007682	NOT AMPLIFIABLE	NOT AMPLIFIABLE	-	NA	-	-	GAATAAATATAT
Ya5NBC319	AC007395	TTGCTGGTCCACAAACCATA	CCTTTGTCATCATGGTGCTG	60	FP	77	358	AAGAATGTATTGTC
Ya5NBC320	AC009498	CCATCTCCCTCATTATTGTTCA	CCATTTGGGAGAAGGTTCAA	60	FP	161	478	CCAAATAGAGTTCTTT
Ya5NBC324	AC008268	TGTCTCAAGGGTCATCCTCA	TCCCCATCCCTAACTCTTTCTT	60	IF	164	486	CTAAGATTCTT
Ya5NBC341	AC007899	ATGCAATTGCTGAACACCAG	GGTGGACCGAGATTTTCTTTC	60	FP	174	494	AAAGAAAAAAGATGTT

(table cont.)

Ya5 485	U67214	ATCATTCTGCCCCTTCACC	CCCAACTTAGGCAACCCTCT	60	FP	180	499	AAGAGTTGCTTTATAAT
Ya5 498[2]	AC007365	AAAATTACAGCAGGCTGAAGG	GGCAGCTGTTAGTTGCTCCT	60	FP	149	460	TATAGAATATTCTT
Ya5 499	AC007561	TCCACCAATTTGAGCTGTCA	GCTGAGCTGGACTTGGATGT	60	LF	133	456	AAAAGAGACATTTCCTG
Ya5 500	AC019226	CTTGGGCACCAGAGCAATTA	AAGAGAAATTTGGGGCTTTC	55	FP	74	376	AAAAGTTTTGGAGC
Ya5 502	AC019100	NOT AMPLIFIABLE	NOT AMPLIFIABLE	-	NA	-	-	AAAAGCTTTTGCATTC
Ya5 504	AC006038	GGAAAAATAGGGGGCCAAAT	CCTTCCCAGCCTTCTCAATA	60	FP	153	486	GAGATATAAAATGTTTA
Ya5 527	AC019181	CCTTGGCTGTCTTCGTGTGT	CTTGGTCAAAGGATAAGAACCA	60	FP	342	678	AAACTTTGCTTTTTA
Ya5 528	AC009482	CCACATGTTCCCTACTTTAGCC	GAACCCATAGCCAGCAAAGA	60	FP	118	436	AAGAGTCAAATAG
Ya5ACA777	AC087073	ACCCCTTTTGGTGTGCTTAT	AACCATGCTCTTATCCCACC	60	FP	130	442	AAAAAGGTGGGATA
Ya5ACA778	AC093616	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AGAAGAGGCAAAC
Ya5ACA779	AC008279	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AAAGAAACATGATCTA
Ya5ACA780	AC009482	TGAGGAAAATTTGGAAAAGA	AGCCAGCAAAGAATAAAACA	55	FP	139	459	AAAGAGTCAAATAG
Ya5ACA781	AC007682	NOT AMPLIFIABLE	NOT AMPLIFIABLE	-	NA	-	-	ATATATTTATTC
Ya5ACA782	AC068970	CCATTAAGCAGTGGTGCCTT	GTTTCATAATTTTACCTTTCCTCA	60	FP	190	466	AAAAGTTGGAGTA
Ya5ACA783	AC079610	NOT AMPLIFIABLE	NOT AMPLIFIABLE	-	NA	-	-	AAAACTATCAGA
Ya5ACA784	AC096772	GAAAGTCCCTCAGGAAACCC	GGGCATACCTTGCTTCAAAA	60	LF	115	431	NONE
Ya5ACA785	AC079300	CCTTTTTCCCTCGGTTTTGT	CCCTCCAACATTTGTCATCA	60	FP	174	498	AAGATACAGACAAACG
Ya5ACA786	AC079452	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AAGAGAAAACCTGTAG
Ya5ACA787	AC068273	CTGGGGTATGTAGGAGGGGT	TCCATTTAGCATTGGGTGAA	55	FP	156	472	AAAGTTT
Ya5ACA788	AC007363	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AAAGAAAAAATATT
Ya5ACA789	AC079607	NOT AMPLIFIABLE	NOT AMPLIFIABLE	-	NA	-	-	AGAAAATGCCCTACA
Ya5ACA790	AC105921	NOT AMPLIFIABLE	NOT AMPLIFIABLE	-	NA	-	-	AAAAAGATTAAGGTAC
Ya5ACA791	AC096552	GGTATCCACTGATCGCTTAC	AGTGATTCTCGGGTTTCAG	55	LF	~230	598	NONE
Ya5ACA792	AC114780	TTTGCTTGGAATCATTTCCC	ATCCCATTACCCTTTCCCAG	55	HF	602	913	AAACCTTTT
Ya5ACA793	AC010906	CTTATCCTGAGCTGCCGACT	GCAAGTGCAAGTTTAAGGGC	60	FP	149	467	AAGAATATTTGC
Ya5ACA794	AC097463	TGTGGCAGTAGAAGCACTGG	TGATGCCTGGAACAATGAAG	60	FP	137	458	AAAAATGTAGATTTTTG
Ya5ACA795	AC011593	CAGATTTCCTTGTTCCCAGC	GAGCGGTCCTGTGGAAAGTA	60	FP	175	481	AGAAATGTTACTCT
Ya5ACA796	AC093865	TGTCAGTGGAGGTGTTGGAG	CCTTTCCCATTTGCATCAGT	60	IF	184	475	AAAATAGCAAGGCCC
Ya5ACA797	AC016691	ACACCTGATGCATGATACCT	ACTGGTTCAGGGAAGTTTTT	55	FP	~364	700	NONE
Ya5ACA798	AC013407	NOT AMPLIFIABLE	NOT AMPLIFIABLE	-	NA	-	-	AAAAATGTATTTATT
Ya5ACA799	AC092843	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	NONE
Ya5ACA800	AC019208	GCATTGCTCCACGGATTAAA	GGCAGAGTTTAAACCAGATGCT	55	FP	171	481	AAAACATTTT
Ya5ACA801	AC019171	CAGCATGAAGCATTAAAGTAGCA	GTTGGAGTTGGGAGTGGAGA	55	FP	164	483	AACATCTGAGT
Ya5ACA802	AC023137	NOT AMPLIFIABLE	NOT AMPLIFIABLE	-	NA	-	-	AAAATGCCATGTG

(table cont.)

Ya5ACA803	AC009223	NOT AMPLIFIABLE	NOT AMPLIFIABLE	-	NA	-	-	AAGACATTT
Ya5ACA804	AC010886	GACCGTGCTTAAGACCCAAA	CATTTCTCTGGGAGTTTGCC	55	HF	158	470	AAAAATCAGCACCA
Ya5ACA805	AC092838	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AAAAGTAC
Ya5ACA806	AC012457	NOT AMPLIFIABLE	NOT AMPLIFIABLE	-	NA	-	-	CAGTTCTGAAGTCTT
Ya5ACA807	AC007462	ATCTTTTTGGGGGCAGTTTT	TCCTGTAGTGAGTTTTGGGGA	55	HF	125	445	AAGAAACAAAAGTTC
Ya5ACA808	AC069550	NOT AMPLIFIABLE	NOT AMPLIFIABLE	-	NA	-	-	AAAAACCTGTAA
Ya5ACA809	AC009600	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	NONE
Ya5ACA810	AC009971	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AAAACTTTACGGGTTTGA
Ya5ACA811	AC079250	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AAAGAAACATCC
Ya5ACA812	AC009971	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AAGAAATACTTCAAG
Ya5ACA813	AC067956	GCCAAAGATGTGAGAAAATCC	AAGTTGTTCATTTGAAAGACGAAT	55	FP	206	500	CCACATATTT
Ya5ACA814	AC080165	TCTCGGGAAATTAGCAATGG	TCAAGAGGCTTTGAGGAAAAA	55	HF	82	423	AAGAAAGAGGGTCTT
Ya5ACA815	AC068542	TGACACCCATAGGCTCCAA	GCAACCTCTGCTCTTTTTGTTT	60	IF	78	389	AAAGAAATGG
Ya5ACA816	AC013722	TTGGTTTTAGCAGACAACCT	TAATGGAGACAGGGTTTCAC	60	FP	269	591	AAGAAATACTAGG
Ya5ACA817	AC008068	TTAAGCTTTCATGCACCATA	AGAATGGTCTCAATGTCCTG	55	FP	385	687	AAAGAAAACTGAAGTT
Ya5ACA818	AC007256	GCTTCTGGCAAGTCTCAATA	CCCAAGTAGATGGGACTACA	60	FP	210	525	AAAAAAATTAGCTGGGC
Ya5ACA819	AC114755	GAAGGAAGCCACAAGCTGTC	CTCGGGGATCTTCAAATTCA	55	FP	479	806	AAAACTGTGGC
Ya5ACA820	AC007253	GGACGAGAAAGCCAGAGAGA	TCTTATCTGCCCCTTTCCAA	60	FP	52	366	AAGAATTGGAAAGGGG
Ya5ACA821	AC010880	TTCTCTTCCCTTTTCTGCCA	TCCAGGAGGACAGAGGTCAT	60	FP	157	475	AAAAGCTACCAATA
Ya5ACA822	AL078621	GCTGGAGCTGGGTCAGTAAG	AACCCAAAGGTCACGGTAGA	60	FP	150	491	NONE
Ya5ACA823	AC021150	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AAAGAAAGGGATGTTT
Ya5ACA824	AC079300	NOT AMPLIFIABLE	NOT AMPLIFIABLE	-	NA	-	-	NONE
Ya5ACA825	AC013469	GAAGACAGGGTTGAAGAATGC	AGGAGCTGATGTCGTAGCGT	55	IF	85	407	AAAAAGAACGTGGAG
Ya5ACA826	AC007677	GAGGCAACATGGAGGTGTTT	AGTCTTCCAATGCCCACATC	55	FP	168	489	AAGAAGAATAAGGGAGA
Ya5ACA827	AC007389	CAGCAGTTTGCAAGCATCAT	TAAAAGCAGATGGGACAGGG	60	FP	626	951	AAGAATTGG
Ya5ACA828	AC018693	GTGAGAACAGAACAAAACAACACA	CCAACTTGAATGCTACCTCCA	55	LF	152	494	AAAGAAATGATTA
Ya5ACA829	AC005234	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	GAAAAAAAGAGAT
Ya5ACA830	AC017083	TGAAGAGCATTCCGAGTGTG	TTCATTGGCAAATCAGTTAGTTTT	60	FP	445	773	NONE
Ya5ACA831	AC074366	GGCTTGCATTTGTCTGGTTT	ACTGGGAAACAAAAGTGCCT	55	FP	100	423	AGACTTG
Ya5ACA832	AC092669	TAGAAAGGCATAAGGGCCAA	AGCCAGTACATTCTTCCCCC	55	FP	138	449	AAGAGTTAAGCCTC
Ya5ACA834	AC010969	CCTGACAACACTAGGGGCAT	TTCTTCTTAATCCCAGGCCA	60	FP	179	488	AGAAAATGGTGGAGCC
Ya5ACA835	AC007681	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AAAGAAATCAAGAAGA
Ya5ACA836	AC096552	TGCCATTGGAAGAACAAAGA	GGAAAATCAGTGCCAGAATGA	55	FP	75	425	AAGAATTCAGTTTTTC
Ya5ACA837	AC092600	TTTCCTGTTCTGTAAAATGGGG	CAGCCTCCAAAGCTAACCAC	60	FP	175	492	AATAGTGGTTAGCT

(table cont.)

Ya5ACA838	AC110614	INSERTED IN REPEATS	INSERTED IN REPEATS		R			NONE
Ya5ACA839	AC105399	TGCGTATGATACACCCTCACT	CTCACACATCATATGGGCAAA	55	IF	174	498	AAGAGTCCAAAATTCCT
Ya5ACA840	AC110614	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AATAAATGAAGCACC
Ya5ACA841	AC017004	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	ATGTC
Ya5ACA842	AC013408	GGCTTTGTTTAGCACACATT	AAGTGCTGGGATTACAAGTG	60	FP	129	447	AAAAATAGAAC
Ya5ACA843	AC092604	TCCTTCCACACTCTTCCCAC	TACAAAATCACAGAGGGGGC	60	FP	162	471	AGAAGATATCTTTCCT
Ya5ACA844	AC016735	GTTTCGTGCCCATTTCTTGT	GGCCCCATCCCTATACAGTT	60	FP	140	442	AAAAATTCAGACTTCTG
Ya5ACA845	AC011746	NOT AMPLIFIABLE	NOT AMPLIFIABLE	-	NA	-	-	AAAGTAGCTTACTTGG
Ya5ACA846	AC068616	GCATGTTCAGCATTTTTCATGT	CATGAAACACCTAAATGTATGAGC	55	FP	166	474	AAGAATTGTA
Ya5ACA847	AC011740	CTGTCCACTGCAGCACTGTT	TCGGTTTGTTCCCAATTGTT	55	FP	55	378	AAAAACAAACAATTGGG
Ya5ACA848	AC079896	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AAAAGTAATATTTTC
Ya5ACA849	AC013262	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	NONE
Ya5ACA850	AC084193	NOT AMPLIFIABLE	NOT AMPLIFIABLE	-	NA	-	-	GAAAATCTTAAAAGGTC
Ya5ACA851	AC009975	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AAGAGTAAAAATATTG
Ya5ACA852	AC104081	TGGGTAAGGACATTTCAGGC	AGCCAGTCCCTTCCTTGAAT	60	FP	110	411	AAAGAAGTGAGCAGAG
Ya5ACA853	AC093162	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	NONE
Ya5ACA854	AC015971	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AGAAAGGTTTA
Ya5ACA855	AC092651	CCATGAGTGTGGGTTCTGTCT	AACCTCTATGCACTGAAAGAAAA	55	IF	141	478	AGAAATTATTTTCTTT
Ya5ACA856	AC012454	CCCTGAAACAAGTGCTCCAT	AGAGGGGACGTCGAGTAGTG	55	FP	105	420	AAAAGCCACTACTCG
Ya5ACA857	AC012671	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AAGAAAGTAGGTCTC
Ya5ACA858	AL353626	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AAAAGACACAGACTGG
Ya5ACA859	AC092835	TGGAGCTTTAGAACAAGCAGG	TGGGCATTCTTTGTTGTCTG	60	FP	173	489	AAAAGGTAATTTTCA
Ya5ACA860	AC019097	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AAGAATGATACATTGG
Ya5ACA861	AC018691	TTGAGAACAACGATCCATGC	TTGGTCTCTGGATTCCTTGG	60	FP	162	484	AAGAAAAATGTTTTTG
Ya5ACA862	AC092587	TCAGAGTAATGCACACAGATGCT	TGCATTAAGTGCTCCAGAAGG	55	IF	149	485	AAAAAAAGTATTTCTG
Ya5ACA863	AC093806	ATTTCCGGATTGGATAGCCT	TGAGAAGTCGAATGGCACAG	55	FP	188	494	ATAACATA
Ya5ACA864	AC016745	GCTGAGCCTTGGTGAAAAAG	TCACTGAATTCCCCTCCATT	55	LF	94	410	ATTAAGGG
Ya5ACA865	AC093393	TCTGGTCCTTTTTGGGTCTT	GCTTGGTTTGAAGTTTGTTCC	55	FP	128	442	AAGAATATGAC
Ya5ACA866	AC068546	GAAAACCACACCAAATTGCAT	CCGCTCTGTAGAAAATGCGT	55	IF	106	426	AGAAATAAAGAGAAA
Ya5ACA867	AC068138	ACCTGCATACTGGCTCAAGA	ATTCACTGAACTCCCCAGAA	55	FP	154	487	AAGACTGCTTAGTC
Ya5ACA868	AC009407	TGCAGGAGTTTTGCTTTCAG	TCAATGTTTCAGCAGGCAAC	55	HF	91	415	AAAGTTTTTTTGCCCTT
Ya5ACA869	AC019130	AGGAAGACCAAAAACACAGGA	ATTATCCAGCTCCCATGTGC	55	FP	153	473	AAGAACTAGCTT
Ya5ACA870	AC079762	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AAAACCAGGTAC
Ya5ACA871	AC007158	CAGTGGTAAAAACACAAATTGCG	TCCTTCCCCTTTGTGACTTG	55	FP	52	404	CACAAATTGC

(table cont.)

Ya5ACA872	AC007404	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AAGACATCGCC
Ya5ACA873	AC010738	NOT AMPLIFIABLE	NOT AMPLIFIABLE	-	NA	-	-	AAGAAAGTCCA
Ya5ACA874	AC079611	AAAATGATCAAGGCGCAAAC	CGTATCCATTTCTCACCGCT	55	FP	62	387	AAACTCTACAGTTGG
Ya5ACA875	AC007252	TGGGCATTCTGAGTACAGGA	GCAAAGGGCTCACAAATGAT	55	FP	168	480	AAAAAAGCAGATATC
Ya5ACA876	AC012065	GGAAGGTATGGGGAGCATTT	GCAATGATCATGCTCAGGAA	55	FP	118	441	ATTGTTTG
Ya5ACA877	AC010895	AAGCCTCCCTGGAAAAGTGT	TCCAAAGGATGTTTGCATGA	60	LF	120	437	AAAGATGAGTAGGAGT
Ya5ACA878	AC010885	CCCCAAAAAGACCAATCAGA	AAAGTCTGTGGCCATCCAAG	60	FP	649	974	NONE
Ya5ACA879	AC016697	NOT AMPLIFIABLE	NOT AMPLIFIABLE	-	NA	-	-	GAAAAATTCCT
Ya5ACA880	AC007037	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AAAAAAAATCTACACCT
Ya5ACA881	AC012363	GAAGACTCAGAGCTGGCAGG	GGGCATAGAGCTTCATTGCT	60	FP	121	449	AAAAAGAGCAGCCTG
Ya5ACA882	AC074392	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AATCAATAGTTT
Ya5ACA883	AC073409	GCTGGATTATTCCTAAATCTGTCC	GCAAATTGCAAATTTCCTCA	60	FP	127	445	AGATAAACTAAGGCTTG
Ya5ACA884	AC079154	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AAAAACTA
Ya5ACA885	AC132153	NOT AMPLIFIABLE	NOT AMPLIFIABLE	-	NA	-	-	AAAAAAAAATTAG
Ya5ACA886	AC073088	AGAAATCATGGTGTGCTCCC	GAGGGTGGAGAAGGGTCTCT	60	FP	89	412	AAAGGATTCAGCCAAG
Ya5ACA887	AC016748	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AAAAATGCACTCATCG
Ya5ACA888	AC013280	TTCTGTTTTGGACAGCCACA	GCCCTAAGCTTCTGGGAGAT	60	FP	128	430	AATTAGCTCCC
Ya5ACA889	AC019050	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AAGAATGTTGA
Ya5ACA890	AC079586	CACAGATAGCTTCGCTGGTG	TGTTGCTGGAGTTGTTTTGC	60	FP	169	473	AAAGATTGA
Ya5ACA891	AC018877	GCCAGACTCCCTCTCTGATG	ATGGTTCCATCTTGTTTGGC	60	LF	158	465	AGAAAAAGAGACGAG
Ya5ACA892	AL356072	NOT AMPLIFIABLE	NOT AMPLIFIABLE	-	NA	-	-	AAGAGTTC
Ya5ACA893	AC092623	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AAAGTGTTGAGCCA
Ya5ACA894	AC012065	TGGAGAAGAAAGGGGGAAGT	GAAGACTCCCTGCCTCAGTG	60	FP	673	999	AAAGAAGTACCGG
Ya5ACA895	AC012595	AAATCACAACTTTTATGTCCCTGA	CATGAGCTAAGTTTTGGGCA	60	FP	170	497	AGAGATCTATACCTGA
Ya5ACA896	AC074391	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AAAAACACTATTGA
Ya5ACA897	AC017082	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AAGAAACCTCAAAATA
Ya5ACA898	AC069394	GGGAACTGGAACCCAAAAAT	ACACTGGGGAACAGAGCAGT	60	FP	507	826	AAGAATTGG
Ya5ACA899	AC110770	ACAAGGGCTGCAACTTCCTA	TTGTTAGCCCTTTTTGAGTAGGTT	60	FP	182	491	AAAAATTTACCTCTTTC
Ya5ACA900	AC012003	CTCTCCTCCTTCCCCACTCT	TCACGTCACTTTCTTCTACCCTC	60	FP	151	477	AAGACAGAAAT
Ya5ACA901	AC110087	CAAGAAAGATCAGCCGTGTG	CCTTTCTCCCTTGATCCTCC	60	FP	164	481	AAAAAGTCCTT
Ya5ACA902	AC078882	GGAACTTGTGCCAGCATGTA	ATGCGCTGGCTATGAACTCT	60	FP	178	489	AAAAAAAGTCAGCTC
Ya5ACA903	AC007364	GGAGTGTGTTCTGAGTGAAAG	TAATGCCACATTCATCTGTG	60	IF	178	499	AAGAAGCAGACA
Ya5ACA904	AC092605	AAAAAGGGAAGCACACATCTC	GGCATACAAAAACATATGCCA	60	FP	92	415	AAGAAGATACTTTATGCC
Ya5ACA905	AC019070	TGTTGGTGTGTGTGTGTGTGT	CAACACTGACAGCCCACTTT	55	FP	112	417	AAAAAAGTGATTTCT

(table cont.)

Ya5ACA906	AC026337	CCTCTGACATGACCATTGTTG	TGGAAAGATCTGCATGACCA	60	FP	177	490	AAATGCACATA
Ya5ACA907	AC009503	TCTCAAGTCCATCCCAGTGA	TGACTGGCTCAACGCATACT	60	FP	166	486	AAAAAATCTTTGGGGTG
Ya5ACA908	AC009227	TTTGCCAAATCTGAAGTGGA	AGTGGCCAACCTCTGCTCTA	60	FP	147	464	GGTATGCAA
Ya5ACA909	AC019186	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	NONE
Ya5ACA910	AC013731	GGAAGAGTGTGGAGGTTATGGA	GTGTGGCAAGGGAAAGAGAG	60	FP	156	474	AAAAACCAGTAAGATC
Ya5ACA911	AC067958	GCAAGCTATTGGACACACCA	CCAGTTAACAGCTTGTGCCA	60	FP	122	432	AAAACCCAGGTCTT
Ya5ACA912	AC010739	CCATGTCAGTAGCTTTCACG	GCCTGACAAAGATGAAACTG	60	LF	74	400	AGTCACCCAG
Ya5ACA913	AC009506	TGCCTATCTGCTAGAAAGGAGGT	AGCCTATGGGAAGTTTTAAAGTAAT	60	FP	169	487	AAAAGTCTTCTGTT
Ya5ACA914	AC064863	AGCATTGCATTTTTGGAAGG	TACATTCTTGTTGCTGGGCA	60	LF	167	491	AAGAATCTTC
Ya5ACA915	AC079258	ACGGATCAACACAGGTGACT	CACAAAGTGCTGGGATTACA	60	FP	80	397	AAAAAGAGGCTGGG
Ya5ACA916	AC009506	TGCATTTTCTCATGCTCCAA	TGGCAATCTATTTTCAGAAGCA	60	FP	76	400	ATTTAATATGAA
Ya5ACA917	AC073046	TGGCCTGTTTTCACACCTTT	CCAAAGCAACTTGCACCTTT	60	IF	171	500	AGAAAAGGTGC
Ya5ACA918	AC019181	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	TAAAAAGCAAAGTTTG
Ya5ACA919	AC016720	GAATCCTAGTGGACAAAGGCA	AATTCTCCCCTGAATCACCC	60	FP	182	495	AAGATAACTGGAAAT
Ya5ACA920	AC011303	GCACAGGTGTTTGGTGTGAT	ACATTTCCATTCCAAGAGGC	55	FP	158	478	AAGAAAACAGTTCAG
Ya5ACA921	AC019086	GAAGTTAATGAGGGTGCCCA	ACTGAGCAGAGTGTATGACCG	60	LF	183	495	AAAAACAATATTTTC
Ya5ACA922	AC019140	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	GAAAAGAGGTTTA
Ya5ACA923	AC011303	TGAGGCTACTACCCCTTCAA	TGGCTGTTCAGAACTTTCAC	60	LF	70	393	AAAGCTCCAGACCC
Ya5ACA924	AC092573	AAGGGTGTGATTCTTGGAG	GGCAATATACGATGTGGAAG	60	HF	377	693	AAAAAGTTAAAGAG
Ya5ACA925	AC093899	NOT AMPLIFIABLE	NOT AMPLIFIABLE	-	NA	-	-	NONE
Ya5ACA926	AC017048	TACCTGCACCTCTGGGACTC	GGCTTCAACCAGGTGAGTGT	55	FP	126	441	AAAAGAAAAGCCCGG
Ya5ACA927	AC016751	AGGCTGCCCTTTCAGACATA	TTGTTCTACCTTGTTGGCCC	55	FP	156	472	AAGAATCGAGTGTG
Ya5ACA928	AC013467	TTTCATCTTTCTAGGCTTCACG	TCCTAGCCATAAATCACAAATCA	55	IF	125	445	GAAAATGAGCTTCTC
Ya5ACA929	AC092162	INSERTED IN REPEATS	INSERTED IN REPEATS		R			TATGT
Ya5ACA930	AC092162	GGTAATGTGGTTTTGGGTGC	CCTGTTGACGTCCTCAGAAA	55	FP	142	461	AAAGAATATGTC
Ya5ACA931	AC017048	INSERTED IN REPEATS	INSERTED IN REPEATS		R			AAAAGAAAAGCCCGG
Ya5ACA932	AC092162	NOT AMPLIFIABLE	NOT AMPLIFIABLE	-	NA	-	-	AAAGAATATGTC
Ya5ACA933	AC010680	TTCAGCGTAAGGAGCAGATA	TCACATGATTTTTGAGCCTA	55	FP	382	696	AAAAAAAATTAAAACTG
Ya5ACA934	AC068196	NOT AMPLIFIABLE	NOT AMPLIFIABLE	-	NA	-	-	AATTTGTTCAATTC
Ya5ACA935	AC068291	NOT AMPLIFIABLE	NOT AMPLIFIABLE	-	NA	-	-	AAAATAACTAAAAATAG
Ya5ACA936	AC093038	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AAAGCCTCCCACT
Ya5ACA937	AC012496	TACTCGTGCAGCAAAATCCA	ACAGCGGAGTGAACGTATCC	55	LF	148	491	AAAAATCCATAAACA
Ya5ACA938	AC009962	CAGGCTTAAAGGCAAACATCA	GATGAGAACATGCAATCACAAAA	55	FP	107	416	AAAACTTCTCCTT
Ya5ACA939	AC096667	CAATCCCAAATCCGAAAGAA	ACCATGGAGAACCTTGATGC	55	FP	67	385	AAGAGATGCATC

(table cont.)

Ya5ACA940	AC021851	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AAAAAGTCAGG
Ya5ACA941	AC023108	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AAAAAACTCCTATATA
Ya5ACA942	AC064871	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AAAAAGATATC
Ya5ACA943	AC093377	GGGAGGGAAACACAAACAAA	ACCCAACTTGACCCTCCTTT	55	FP	115	429	AGAAAAG
Ya5ACA944	AC019178	GGGAGTCTAAGTGCTCTTGAAAA	TTTGGAAATAACAGGATCCACA	60	FP	137	452	GAAAATATACTAGTA
Ya5ACA945	AC092162	NOT AMPLIFIABLE	NOT AMPLIFIABLE	-	NA	-	-	AAAGAATATGTC
Ya5ACA946	AC006460	CAGCCACTTCTTAACCAGCC	CAACACAACACTGGTAGGCA	55	FP	152	462	AAGAAAAATGCC
Ya5ACA947	AC092598	GATGGAGGTGTATTACAATGGAGA	GAAGGGTTCAGTGTGGAAGC	55	FP	128	435	AATGGAGATCAA
Ya5ACA948	AC013475	ATAGCCTCTTGGGCCATTTT	TTGGGAAGGTCTTTTCAAATGT	55	FP	174	482	AAGCAGGGTC
Ya5ACA949	AC013475	CTTTGGTGTTTGCCAAAGTT	TGGCACAATTGAAACAGGAG	55	HF	136	476	AAGATATTTCTCATT
Ya5ACA950	AC053523	GCTCCAGGTAGAACCAATGAA	GCATAAAAACATAGAATGCAAAGC	55	FP	159	475	AGAAATAGTTTACTT
Ya5ACA951	AC068135	TCATTAGCTTGTGTACTCTAAAGG	AAGTTTGCAAAAACATTGTG	55	FP	90	437	AAATTTTGA
Ya5ACA952	AC006196	GGAGGTGTAAGCTCTCATTTCCT	GACAGATTGAAGGAGGCAGC	55	FP	138	450	AAATATGTATCCCTC
Ya5ACA953	AC068919	GCTTTGCAATTCTTTTGGCA	TCACTTTGAACCAGTTTCCCTT	60	IF	171	450	AAACTACTTAAGGGAA
Ya5ACA954	AC016711	ATCACTCTCCCCTTCAATTT	GTTCTGGGATTACAGGAGTAAG	55	FP	178	499	AATACTATAGGCTGGG
Ya5ACA955	AC074290	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	ATTATGAATACCT
Ya5ACA956	AC053523	TGGTTATTTTAATCCAGGCCA	ACGCATACGTGTGTGGTTGT	55	FP	153	462	AAAAAATCAGAAAACAG
Ya5ACA957	AC013475	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AATAAGCTTAAGGA
Ya5ACA958	AC023430	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	CAAATCTTGA
Ya5ACA959	AC020550	CAAAAAGGACAAATGCTCCAA	CCACTATGTGGATTTTCCCAG	55	FP	160	484	AAGATTGTATCTGTC
Ya5ACA960	AC074090	GCTCAAGAAATATGTGCCACC	TGAGAATATCATGGGATGGCT	60	FP	165	454	AAATATGTGCCACCA
Ya5ACA961	AC073417	CAGGCACATGCACAGATACA	CCAAAACAGATTGGCAAACA	55	FP	194	495	AAAAACAATTTTC
Ya5ACA962	AC011997	GGCTGTTGCCAGTAGAAAGC	AGACGGAAGTGACAGACAGTGA	60	FP	152	442	AAAAATCCTTACCTTT
Ya5ACA963	AC016903	GGCCTGAGGTATTGTAAAGATT	TGTAAAAGAAGGCATCGAAT	60	FP	163	500	AATGCAAAGCACTG
Ya5ACA964	AC007272	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AAAAGTTGATTT
Ya5ACA965	AC007005	CAGCCAGACTGTAGCAATGTC	TTGGGCAAGTTAACCTCACTG	55	FP	127	443	AAGAAAAAAGCA

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Ya5NBC51	AC008249	ATATTCCAGAAGTTTCCTTACATCTAGTGC	AAAGCTTTAAGTCTCCACCATCTCT	60	IF	140	437	ATGCTTTG
Ya5NBC112	AC008032	GGTTATTAGTTTTGGGGTGGTAGTC	GGGATACCCAATTCAGTTGTACTAG	60	FP	93	396	AGAAAATCTAG
Ya5NBC181	AC008041	GTTACAGTGCCTACTTCTGGTTCTC	AGCCTTCCATCCTCATAGACC	58	FP	204	450	TACAATTTGCATTTT
Ya5NBC312	AC01069	CACTCAGCATCCAGTTCACG	GGCCTCTGGTTTCAATTGTC	60	FP	54	365	AGCTTTT
Ya5 478	U67225	TGTGTGGGCAAGAAAAGAGA	ATGCACACATTGCTTGTGCT	60	FP	234	553	AAAAAGTGAGAATC
Ya5 488	U67209	TCCAATACCTGACTGAAATCCA	TGGTTCTCATGGAGCAAGGT	60	FP	146	458	GAAATATTCACAATTGT

(table cont.)

Ya5 519[2]	AC034195	TGGGTTAGGTTTTTGCTTGA	TGGAGTGAAATAGTGTGTGAAACC	55	FP	84	398	AAGTTCTTTCA
Ya5 520	AC018507	GTTGGAACCAATGGCCTTC	TCCCAAGAGTGTTGTGATCG	55	FP	181	517	TAACAATGTCTGATTTT
Ya5 522	AC012087	AAGACACTGGCCCATTTTTG	TCCAATCTCTTGGGGCTCTA	60	FP	121	438	AAAGAAAGAA
Ya5 532[2]	AF245699	TTTTGCCCTTCTCGTCAAAT	GTATCCTCGGGGAGTTGGTT	55	FP	105	418	CGGAAAATTTTTTT
Ya5 534	AC007920	CCACAAAGCAGAATGTAGAAGG	AGCTGGGAAATGGTCACAGT	60	FP	93	412	NONE
Ya5 540[2]	AC016950	AGCCAGTAGCTTTGCACACA	AGATCACGCACCCTTCACTT	55	FP	120	445	AAAAAGAGACT
Ya5ACA966	AC119038	AGGATCCCATTTCCTTCCTC	GCCTGTTGCTCATTGTCATC	55	FP	624	939	AGAAG
Ya5ACA967	AC104445	NOT AMPLIFIABLE	NOT AMPLIFIABLE	-	NA	-	-	TTACAGAAG
Ya5ACA968	AC092942	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	TTAGC
Ya5ACA978	AC069219	TCATGGGGAGATGTTGACCT	TCTGACAATCTGTAAGCCCAA	55	FP	75	390	AAAAAGAGTATTGGG
Ya5ACA979	AC104302	TATGTTGCCTGGAAAAAGCC	CCTACTTCCTTCATCGGCAA	55	FP	115	457	AGAAAGGACCTTAGAC
Ya5ACA980	AC108670	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	NONE
Ya5ACA981	AC093416	GCAATTGCTCACAGTACTCCA	CAATCGTTAGTCTCAACGCAA	55	FP	127	428	AATAATAATT
Ya5ACA982	AC011325	NOT AMPLIFIABLE	NOT AMPLIFIABLE	-	NA	-	-	AAGAAAGAGCGCATAG
Ya5ACA983	AC093025	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AAAAAAAACAAATTT
Ya5ACA984	AC018828	NOT AMPLIFIABLE	NOT AMPLIFIABLE	-	NA	-	-	NONE
Ya5ACA985	AC079623	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AAAAAAGG
Ya5ACA986	AC079623	CCTTTCGAAAAGTGTCAGGC	AGCACAGTTGCAAAATGCAC	55	FP	118	432	AAAAATTATTTCCTT
Ya5ACA987	AC078877	TCACTGGTCTTTTATTTGTGGC	TGGTCTCTCACACATGCACA	55	FP	182	493	AAAATGAATGTATAC
Ya5ACA988	AC078980	NOT AMPLIFIABLE	NOT AMPLIFIABLE	-	NA	-	-	AGAATGATAAAAATAG
Ya5ACA989	AC105753	NOT AMPLIFIABLE	NOT AMPLIFIABLE	-	NA	-	-	AAAAGTATAGAGGAC
Ya5ACA990	AC092910	GGGAACTTTAATTGCCTTATAAAAA	CCCACAGCTTGCTAACAGAA	60	FP	157	474	TTATTGCA
Ya5ACA991	AC007920	NOT AMPLIFIABLE	NOT AMPLIFIABLE	-	NA	-	-	NONE
Ya5ACA993	AC112128	GCATGAAAATAACCATAGGC	TATGTAAATGTGGTGGGTCA	55	FP	158	468	AGAAATATTCACAATTG
Ya5ACA994	AC130473	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AAGAACATGCGG
Ya5ACA995	AC069506	GGCTTTAGCCACATCCTAATTT	TCCTTCATTTCTGGGTTCCA	55	FP	143	460	AAGAACACACC
Ya5ACA996	AC099052	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AAGAGTCTTTTCA
Ya5ACA998	AC092047	ATATTGGGGCCTCTGGTTTC	AAACCCATCACTCAGCATCC	55	FP	69	380	AAAAGCTACCGTG
Ya5ACA999	AC124045	ATAGGGAGGTCGGCTGTTTT	TCCTTCAAGGGACACTGGTC	55	FP	226	457	AGAAAATCTAG
Ya5ACA1000	AC138069	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AAGAAGAAAACAC
Ya5ACA1001	AC132807	TTCTTGCCATACCAATAGCTG	AAGGAAAAAGCAAGAATGAATCC	60	FP	169	475	AAAAGAGTTCCA
Ya5ACA1002	AC104451	GGGGTTGGAGAACCCTGTTA	AAGGAGTAGATTGTGATGGCCT	60	IF	132	457	AAATATGGCTATTTTTA
Ya5ACA1003	AC132807	AGGGTCATCGTCAGGACAAG	TAGAGGCCCATTCCACAGTC	55	HF	637	957	AAGAAGTATGGTGTC
Ya5ACA1004	AC090952	CACATGAGGTGGTCGTCAAG	GAGCCTCACAGGCTTACCAG	55	FP	174	486	AAGACACAAGCTAG

(table cont.)

Ya5ACA1005	AC083855	GGCCAGGAACGTAATCTGAA	GGTTCCTTCTCTCCCACCTC	55	FP	122	444	AGAAAGGATTACTGCA
Ya5ACA1006	AC016961	CATCAAGAAAGACCCTCCCG	AGGCTGATGCGTTGTGATTA	55	FP	150	481	AAGAAAGACCCTCCCG
Ya5ACA1007	AC055711	NOT AMPLIFIABLE	NOT AMPLIFIABLE	-	NA	-	-	NONE
Ya5ACA1008	AC069226	TGTCTTTCAGAGAAACATTGGAAA	TTCCATGCACCCAACAGTTA	55	FP	150	456	AAAATGGAATGG
Ya5ACA1009	AC091493	GCCTTTTAAAAATGGATTCCC	CATCTGTCAATTCGATGACCA	60	FP	90	406	AAAAATGGATTCCC
Ya5ACA1010	AC092969	TCTGAGGGCTAAGACCAGGA	CTGTTCTGCTGGGCACTGTA	55	FP	313	491	NONE
Ya5ACA1011	AC020631	CGGTCCCTGACCATAGATGT	AAGCAGTCAGTGTGCAGCTC	60	LF	185	500	AAAAATATTTG
Ya5ACA1012	AC092039	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AAAAATCATAATGAG
Ya5ACA1014	AC104162	GTTGCATTTTGGTGGGGATA	CAGGGGGCAGTGATACTTTC	60	FP	163	493	AAAGTAATTGTC
Ya5ACA1015	AC114877	AGCAAGACTTCGTCTCTCTCT	ACTCAGTATTGGGAGAGGTG	60	FP	148	460	AAGATACATGAG
Ya5ACA1016	AC096922	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AAGAAGCACTAGG
Ya5ACA1017	AC092937	CATGAAAGAGGGAAAACAAG	TTAGCAGGTTCCTAGGATAGTC	55	FP	246	568	AAGAAATA
Ya5ACA1018	AC026671	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AAAGGCC
Ya5ACA1019	AC107623	TGCCATAAAGAAATGGGGTT	TTCAAAATATGCACTCTTCACCA	55	FP	165	483	AAAGAAATGGGGTTAA
Ya5ACA1020	AC104330	AATCGCCTTCACTTTTCTG	CAGCAAGGAAAGAGGTAGAA	55	IF	81	377	AAAAACGAAGACAGTA
Ya5ACA1021	AC131154	TTAACACCTCTGCACTTTGTGAA	ACGGCTCCCAATCAATTTAG	60	FP			GAAAAATACCTC
Ya5ACA1022	AC130004	TTGACATGTGAAATGCAAAACA	TCCCAAAGGCAAATCAGAAC	60	FP	148	468	AAATCTGGTTTGC
Ya5ACA1023	AC108700	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AACATTGAGGCAG
Ya5ACA1024	AC107302	GGAAAGGAGCCAGAATAGCC	CAAACATCTCTGGGGAGAGC	60	IF	156	470	AAAAATGAGTACCTGTG
Ya5ACA1025	AC112223	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AAAAGAATAGGGGCG
Ya5ACA1026	AC119034	TCTTGATGTCATATTGGGCA	GGTTTCCTGGAATCATGACC	55	FP	57	366	AAAATGGGTCATGA
Ya5ACA1027	AC023127	NOT AMPLIFIABLE	NOT AMPLIFIABLE	-	NA	-	-	AAGAAAATAGAAGTC
Ya5ACA1028	AC068757	TGGTTTGAACAATTTGCTGG	GGGAGCACACATACACCCTT	55	FP	135	481	TTTCAGGTATG
Ya5ACA1029	AC099059	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AAGAACAAAAGCATTCCT
Ya5ACA1030	AC068757	NOT AMPLIFIABLE	NOT AMPLIFIABLE	-	NA	-	-	TTTTCAGGT
Ya5ACA1031	AC108715	CCACAATAAACACAAATTGC	ATTGTTCTGTCCATCCATGT	55	FP	101	381	AAAAAGATGTGAGGGTA
Ya5ACA1032	AC104186	NOT AMPLIFIABLE	NOT AMPLIFIABLE	-	NA	-	-	AAGAAAATGTGAACATA
Ya5ACA1033	AC024218	TTTTCCAGCCATGACCAAGT	CACCACAAATTTTGGATTCATTT	60	FP	189	500	AAAAGTAAATGTC
Ya5ACA1034	AC021660	AAGGCTTTAAGAAAACGCTGT	TTTTCTTAGCCCAGTCTTGGA	55	FP	133	450	AAGAAAACGCTGT
Ya5ACA1035	AC021064	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AGAAAAATAAAACTA
Ya5ACA1037	AC069529	NOT AMPLIFIABLE	NOT AMPLIFIABLE	-	NA	-	-	CAACATT
Ya5ACA1038	AC020651	ATGGCAAGCAAGGAAATTGA	CACCCATCTTCCCAACTGAT	55	FP	166	492	AGAAGTGCTTAGATTTC
Ya5ACA1039	BC027207	CCACTTGGATGGGAAGGTAA	AAGCACGTCACACCCCTAAC	55	FP	50	372	AAAAGCGTTAGGGGTG
Ya5ACA1040	AC124045	CATCGCCATCTTACAGACAA	AACTGTGTGACACTGGTTGAC	55	FP	65	298	AGAAGTTAA

(table cont.)

Ya5ACA1041	AC078811	CAAAAGTAATTGTGGTTTTGC	GGTTGCTTAAAAAGTAATTGCAG	55	FP	65	513	GAAAGTAATAGCAA
Ya5ACA1043	AC073360	ACTGGTAGCTGCCCATGTCT	GGAGCCTACCTCTTTCCGTC	55	FP	138	461	AAAAGAGAACAAAG
Ya5ACA1044	AC078952	CCAAAACACAATAGAGGAGCTA	TTCTACCACCCCAAAAATGT	55	IF	233	552	AAGCATTCTC
Ya5ACA1045	AC078980	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AAAAGAGAACTACC
Ya5ACA1046	AC074044	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AAGAAAATGACAGG
Ya5ACA1047	AC092909	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	NONE
Ya5ACA1048	AC080006	ACCACGGTATGACCCACACT	GCTGATGCTACTGTTGTCACCT	55	IF	413	715	AAAAAACACAGG
Ya5ACA1049	AC005923	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	TACAAAAAAAAT
Ya5ACA1050	AC104166	AAGGCTTCCATCTTTCCTCT	AAACCACAGGGACTTAATGC	55	IF	108	399	AATAAAATCCA
Ya5ACA1051	AC117430	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AAAGTATAATTTA
Ya5ACA1052	AC099544	TTTCTTCAGGAGCTCTTTTG	CTCAGCAGAAACCCTACAAG	55	LF	199	493	AAGAATGTTGA
Ya5ACA1053	AC098972	TTTTCTGGATTCTGTTTCCAA	CCAATTCAAATAGTTGCCCC	55	FP	162	467	AAAAATTGTGG
Ya5ACA1054	AC114400	ACATTCTCATCTGGGGCAAG	GCTGCTAACAGGAATCACTGC	55	HF	153	480	GAAGATCTTTG
Ya5ACA1055	AC099538	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AAAAGTGAGTTCAC
Ya5ACA1056	AC133124	TTGCTGTGATTTTCGTTGGA	GGGAATTAAGTTAACCACATGCT	55	FP	138	449	AAGAGTGACTAGC
Ya5ACA1057	AC012557	CTTGACACCTGCTGTGAGGA	CGTGAAGTTAATTGCTGCCTC	55	FP	145	453	AAGAAAAGGAGG
Ya5ACA1059	AC092952	NOT AMPLIFIABLE	NOT AMPLIFIABLE	-	NA	-	-	NONE
Ya5ACA1060	AC112516	GGACAACATGCTTGATGCAG	GCCCACTTTTCAAATGAGGAT	60	FP	162	483	AAAGAGGTGGGATG
Ya5ACA1061	AC020631	NOT AMPLIFIABLE	NOT AMPLIFIABLE	-	NA	-	-	AAAGAATACA
Ya5ACA1062	AC016959	TCAAATGGAAGGCTAGGACG	TCCCTTCTGGTGTGTGAGTG	55	FP	72	372	AGGAAGGCGGGCACTC
Ya5ACA1063	AC092902	CCCTTTATGAGCAATGCGAT	CTATGCCCAGCATTTTTCA	60	LF	157	466	AAGACAGTACA
Ya5ACA1064	AC130566	CTGGGAAGCAGGAACAACAT	CATTAGCCCCCAGTGTCATC	55	FP	181	491	GAAAATAGCTTAATCT
Ya5ACA1065	AC055752	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	NONE
Ya5ACA1066	AC108688	ACCATAATCCTCTCCCATCT	TACTTTGGCTTTGGTTGATT	55	FP	271	590	AAAATGTCCATGATG
Ya5ACA1067	AC020631	TCACAATGTAAAATGCTTGC	GCTCATTTGCCTATTAGCAT	55	FP	114	400	AAAGAATACA
Ya5ACA1068	AC134027	CACCTCTTCCCACTTTGGAG	CTACAGGGTCCAGGCAGGTA	55	FP	92	416	AAGAGAGGCGCTGGT
Ya5ACA1069	AC093004	AGAAAATCTGGGCCTCAATG	AACGTTGGGCAGACAAAATC	60	FP	141	452	AAAACATCTTA
Ya5ACA1070	AC023593	CGGATCCCTCAAGGATGATA	TCCCCAGCTGACTTCTGTCT	55	HF	120	442	AAAAAGTCAGCTG
Ya5ACA1071	AC104450	CTGGGCAACATAGTGACA	TCTGTCTGCCACCTAGAAAT	60	IF	75	366	TTAAA
Ya5ACA1072	AC135002	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	TTAAGTAAAGC
Ya5ACA1073	AC055753	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	GAAACTCACTCA
Ya5ACA1074	AC076961	CCCAAGGGCTTCTTTTAAGC	AAGGCAATTGCAAAGCAGAT	55	FP	86	403	AAAAGGCTGATCTG
Ya5ACA1075	AC117409	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AAAGACTTAAACGT
Ya5ACA1076	AC016919	AAACAAGCCTCGGTCTTTGA	ATCTTGCAGACACGTGCATC	60	FP	139	463	AAAGCTCTGTGTTCTG

(table cont.)

Ya5ACA1077	AC135002	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-		AAGAACTACTGCAGG
Ya5ACA1078	AC016252	NOT AMPLIFIABLE	NOT AMPLIFIABLE	-	NA	-	-	AAAAGGCCTTGAGGG
Ya5ACA1079	AC007159	GGAGGGGAAAGACATTGGAT	TTTGCATATGTTGGGCTTGA	55	FP	176	482	AAGAATGCTGCTCTGG
Ya5ACA1080	AC007159	AAAGCCTTATTCCTGCTCCC	ACGCCCAGGTAAGGAGACTT	55	FP	174	485	AAATTTGTACTGAG
Ya5ACA1081	AC026324	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AAAGAAAATAAAATACG
Ya5ACA1082	AC117390	GACTTCTGTTCAGCTTTGCACT	TGCAAATGATTTTTGCATCC	55	FP	212	500	AAAAAAAAGAAAGAA
Ya5ACA1083	AC133435	GGGGGTGCTCTCCTATTTAGA	CAGGGGCTAGATATGGTCACA	60	FP	111	426	AGAGAACACGGGAATA
Ya5ACA1084	AC108727	CAGCAAGTTTGTGGTAGAGCC	CTGAGAGGAGCAAGGTCTGG	60	FP	157	473	AAAAGACAGAAGGA
Ya5ACA1085	AC092958	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AAATTTAAATAT
Ya5ACA1086	AC021059	TCTTTCAGAGGCCCCTTTTT	GTGGTCAGCTACCTTTTGGG	60	LF	405	76	AAGATGCAAAAATA
Ya5ACA1087	AC108699	ACAGAGCAAGATTCCGTCTC	GGTGCAGGTTAGTTGTTTTC	60	FP	101	388	AAAAGAATTATA
Ya5ACA1090	AC013251	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AGAAATATAACTGAACT
Ya5ACA1091	AC016142	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AAGATTACAGAGAGAC
Ya5ACA1092	AC117395	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AAAAAGTTCACATATT
Ya5ACA1093	AC018449	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	ACAGCTTTTA
Ya5ACA1094	AC105749	TCTGCTTTCTGTTAGAATCCAGTT	GTGCTGTGAGGTTGGGATTT	55	FP	107	420	AAAAACCCT
Ya5ACA1095	AC107030	AGAATGCAGCTCGTTCCAGT	TGGGGAAAATTCATTTCGAG	60	FP	137	468	NONE
Ya5ACA1096	AC104472	NOT AMPLIFIABLE	NOT AMPLIFIABLE	-	NA	-	-	NONE
Ya5ACA1097	AC092994	GGCCACAAATGCAGTGTTTA	TCTCCATGCCCAACTCCTAC	55	FP	127	451	GCAGTGAAAAA
Ya5ACA1098	AC110152	CCAAACTAGGTCCTTCAAAAACA	ATTCAAGCCTCCATGACCAC	55	FP	146	464	AAACTAT
Ya5ACA1100	AC073359	GCATCCTACAAAGCCATT	GCCTGGGCAATAATTTTCAA	55	HF	170	492	AAAAGAAATAAGGTT
Ya5ACA1101	AC073359	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	TAAATT
Ya5ACA1102	AC095349	CAGCCACCATTCAAAGAAAA	CATTTGACTATTTCATCAACAGCC	55	FP	172	479	AAATAAACTATT
Ya5ACA1103	AC021654	AAAGATAGCTGGCTGGGTA	GGCTAAAAACAGTACCTATGCT	55	FP	~310	702	NONE
Ya5ACA1104	AC128694	TAGAGGCCAGGCTTAGTGGA	TCTGCATCCTAATTGTGGTGTC	55	FP	155	472	AAAATGTTTTCC
Ya5ACA1105	AC104471	NOT AMPLIFIABLE	NOT AMPLIFIABLE	-	NA	-	-	TTCCT
Ya5ACA1106	AC112491	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AGAAGGTAAGATTAGGG
Ya5ACA1108	AC117459	GAGCACATATGGGTAGTAGATCC	TTGCTCGTCTTGATAACTTTG	60	FP	270	592	TCAAAAAATGTGTAAA
Ya5ACA1109	AC018360	GATCAAAATGTGCCCAATGA	CAGGCTCCAAGGACACTTCT	60	FP	142	441	AAAAGCAAGTT
Ya5ACA1110	AC108698	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AAAAAGATGTGAGGGTA
Ya5ACA1111	AC073288	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AAGAATAATGCTGCTATA
Ya5ACA1112	AC079822	TGCAGGACTAAGTGTGTGGC	TCAGAACATGACTGTGGACATTT	60	FP	124	437	AAAAAAGTATTTAA
Ya5ACA1113	AC007849	NOT AMPLIFIABLE	NOT AMPLIFIABLE	-	NA	-	-	AAAAAGGAAAGGG
Ya5ACA1115	AC069243	GAACAGGGCTTGCTCAGAAT	AATACCCTGGTAATTGGCGG	55	FP	107	417	NONE

(table cont.)

Ya5ACA1116	AC107311	TTGGACATCATCCTGCAGTT	GGCGGCGTATAGCAATTATG	60	FP	139	454	AAAACTTCCTT
Ya5ACA1117	AC073288	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	NONE
Ya5ACA1118	AC055714	GCCCTTAGAAACCCTTGCAT	ACTCCAATAGGAAGGGGAGC	60	FP	142	449	GTCAACCT
Ya5ACA1119	AC008134	GGGGTACACACAAGGGAATG	GGGGGTTCTAGCTCTCTTGC	60	FP	128	465	NONE
Ya5ACA1120	AC092967	ACTGTGCTGCCTTTGTTTCA	ATCCGCACACCCACTTTTAC	60	FP	107	416	AAGAAGAGTTTTC
Ya5ACA1121	AC012082	CAGGAATGCAATATGCAAGG	CACCAACTGACAGGAAACCA	60	FP	84	402	AAAACAAGGACTTG
Ya5ACA1122	AC069418	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AAAAAAAGAATGAGATC
Ya5ACA1123	AC112510	ATATTTTTCCTACCATCAAAAC	CACCCTGTCTATAACTTCAAAA	55	FP	80	399	CAATACTC
Ya5ACA1124	AC092923	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AAAGAAAATG
Ya5ACA1125	AC063953	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	NONE
Ya5ACA1126	AC055714	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AAAAATCACTAGC
Ya5ACA1127	AC069259	CCCAGCAGTCTCACTTAGCC	GCCCCATCTAGCTGAATCTG	60	FP	164	479	AGAATCCAAGGCCTTC
Ya5ACA1128	AC055723	CCAAAGCTTTCTTTGTAGCAGC	CCCCACCGGAAATATACACA	60	FP	126	439	TTTGTG
Ya5ACA1129	AC078981	GAAGCAGAATATCAGGGAGAGG	GCCAGCCACCATAAGTCTTC	60	FP	72	398	NONE
Ya5ACA1130	AC092963	AAATGCCTAGTAGGAAAAAGGGT	TCCTTCCCTGCATTCATTCT	55	HF			AAAAAAAAAAGAAATT
Ya5ACA1131	AC117415	TAATGGAGCTAGGTCCGGC	TGTACCTGTTTTCCTGCTGCT	60	FP	125	467	TGATATGAAGTCT
Ya5ACA1132	AC068760	AGTGCCACTTTGAGACCCTG	TGCCTTTCTCCTCCAAGATG	60	FP	179	484	AAGAAATGTT
Ya5ACA1133	AC036127	NOT AMPLIFIABLE	NOT AMPLIFIABLE	-	NA	-	-	AGAATGCAGACTA
Ya5ACA1134	AC104452	TCCACCTACCCAAGTTTTGC	GACAGCGCTCAGTGATGGTA	60	LF	146	475	AAGTTACCATC
Ya5ACA1136	AC099056	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	TACATT
Ya5ACA1137	AC063919	ATTCCATGAAGGTTTGCCAG	CCACGTCCTCCTCCATGTAT	60	FP	75	402	AAGAATACATACATGG
Ya5ACA1138	AC104452	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	NONE
Ya5ACA1139	AC116991	TGGGGACTCCTGTTATTAAA	AAATGTTGTTGGCAGATTTT	55	FP	79	393	AGGCAAAAATGG
CHROMOSOME 4								
Ya5NBC61	AC009594	TGAAATAATCCAGTTGGGGAAG	GTATATCTCTACCGAGACTCAGTTT	55	IF	180	493	AAAAAAATCCTCCTT
Ya5NBC69	AC004053	GGGATCAGTTACAGTGCTTC	ATGCAACGCAACTTAGAACT	50	FP	42	359	CAGTGCTTCATAGTTCT
Ya5NBC70	AC004454b	ATCAACGTGGGACATAACCA	TTCAGAAGGCACATTAGTGCT	60	FP	116	391	CTATTAATATACTCTT
Ya5NBC73	AC004454a	GACTATTAATACGAATCCAAAGTACACG	TTTAACTTGGTCCTACCTGTGTGTC	51	FP	129	465	CAAGTCTCTCATTTCTT
Ya5NBC163	AC004057	CAAACCAAGAGTTCTTATCACCAGT	TAGTAAGAGGTTTCCAAAGTACACG	60	FP	316	624	GAGGCTATTTTTT
Ya5NBC185	AC006552	GAGTTTATTTGCCGTAGGTAGCTC	GGTAGGGGCTAAATGGAAAACA	61	FP	202	513	AAAAATACACATTTCC
Ya5NBC198	AC004055	GCATAACTCCTAACCCATAATTTCC	GATCTAACACAACCAACTCCATCTT	60	FP	230	530	AAATCAAGCTC
Ya5 430	AC004047	TTTCATTCCCTGCTTCCCTA	CACATTTCCTTCAAGAGGTCAA	60	FP	490	800	AAAAAGTCAG
Ya5 476	U67227	TTTTCCAGACATCATTGTGC	TCAGGACAATTTGGAATGCT	60	FP	245	556	AAAATG

(table cont.)

Ya5 525	AC012055	CAAAAGACATAATCAAGAAATGAAAA	TGGAATCCAAAATCGTGCTT	60	FP	240	530	AAATTTCATTTCTT
Ya5ACA1141	AC021193	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	GAAATGCTACACA
Ya5ACA1143	AP001820	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	TCTTGGCC
Ya5ACA1144	AC017063	NOT AMPLIFIABLE	NOT AMPLIFIABLE	-	NA	-	-	GAAAGTACTGGATTA
Ya5ACA1145	AC092458	GGAGGTTTGAGAACTGACCG	CCAATCAAGCTTTTCTCCCA	55	IF	400	719	NONE
Ya5ACA1146	AC067946	NOT AMPLIFIABLE	NOT AMPLIFIABLE	-	NA	-	-	AAAAATATCATTTGTG
Ya5ACA1147	AC053527	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	ATTTAATAA
Ya5ACA1148	AC096721	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AAAACTGTATTATA
Ya5ACA1149	AC018710	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AAAAAAAAATTCTGGGT
Ya5ACA1150	AC053544	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AAGAGTGTTAAGG
Ya5ACA1151	AC020734	NOT AMPLIFIABLE	NOT AMPLIFIABLE	-	NA	-	-	NONE
Ya5ACA1152	AC093854	TTTCCAGACATCATTGTGCC	CCTGAATGTAGACCCAGACAGA	60	FP	155	470	AAATCCAAAAAATG
Ya5ACA1153	AC021539	GGCAGGAGTTAGCCAGGTAG	CCTGGGTTGTCCTTCTGTGT	60	IF	-	-	AAGAAGACACAG
Ya5ACA1154	AC074194	CAGTGGTGTCCCCTGAAGTT	AATGCGCGGTAACATACACA	60	FP	514	832	ATTTTGT
Ya5ACA1155	AC104656	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AAAAAGTCAAGAAAC
Ya5ACA1156	AC097711	CCGTCAAAACTTGAGAGATCC	CCATCCCTACTCCTGGTGAA	60	FP	91	408	NONE
Ya5ACA1157	AC027607	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AAAAAGGTGTG
Ya5ACA1158	AC105400	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AAAATAATTGTTTCA
Ya5ACA1159	AC093736	TCCTTCACGTAGTTCACGACA	CAAGTGTCCAGTTGACAGGAGT	60	FP	172	491	ATTTC
Ya5ACA1160	AC092597	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AAAAGGGACCCCA
Ya5ACA1161	AC017091	AGTGGGAATCACTATGATGG	GTCTTGACCTCGTGATCTGT	60	HF	159	479	AAAAAAGACAACACTG
Ya5ACA1162	AC093848	GCTTGCTTCTTTCCACCTCA	GCCTTCAGCAATACACACCA	60	FP	114	436	CATAGGCAGGA
Ya5ACA1163	AC068620	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	TAAAATTAACTT
Ya5ACA1164	AC095061	CGGGGAGAAGGTCAGTGTAA	CCTGACGTTAAATCACGTAATCA	60	FP	75	388	AAAGATTATGTGA
Ya5ACA1165	AC097661	AAAGGGAACAGATCCAGGAAA	TTTGGTACTTGGCAAAACCC	60	FP	170	489	AAGAAAAAAGAGAG
Ya5ACA1166	AC079772	CATTTCCAGATAAGCCCCAA	TTTCAGTGATTTTCTTCTTTCTT	55	FP	105	430	AAAATCACTGAAATA
Ya5ACA1167	AC104656	INSERTED IN REPEATS	INSERTED IN REPEATS	-		-	-	AAAAAGTCAAGAAA
Ya5ACA1168	AC096721	TGCCTTATACGGTTGTTAACCC	TTCCTTTGCTTTCTGTTACCTG	60	HF	214	493	AAGAAAAACAAACAA
Ya5ACA1169	AC097489	GTGAGCACTTCAGGTACGTT	ACTAACGTGCTCTTCTTCAAA	55	FP	145	468	AAGAAAGCCTACA
Ya5ACA1170	AC104805	NOT AMPLIFIABLE	NOT AMPLIFIABLE	-	NA	-	-	NONE
Ya5ACA1171	AC021860	TAAGGTTGAAAGCTTTTGCT	ATTGTGCAACCCATCCTA	55	FP	50	378	NONE
Ya5ACA1172	AC093844	CTCTCCACCAACAAAGAATC	TGCTAGGATTATAGGCATGAG	55	LF	176	499	AAAGAAAGTGCTATGTT
Ya5ACA1173	AC093790	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AGAATTCTA
Ya5ACA1174	AC023886	CAGGCCAAAGTTCTTCACAA	TGGCATGCTGCTATAATGTG	60	IF	189	496	AAAAATGTAAAGATG

(table cont.)

Ya5ACA1175	AC004057	CTTCAGGCCAGGAGTTTTGA	AGGAAGAGAGCTCCCCTGAG	55	FP	124	459	AGAAAAG
Ya5ACA1176	AC093879	CGGTAGGAAAATTTGGCAAG	AAATTACTGTCAAAGAGGCACACA	60	FP	62	378	AAAATGTGTGCCTC
Ya5ACA1177	AC024230	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AACAGATGTCCAA
Ya5ACA1178	AC097489	CTTGGGATTGTGAGGGACAT	TGAAAGCCATGCAACTTTTG	60	FP	186	498	AAGTATATG
Ya5ACA1180	AC110615	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AAAAAACTG
Ya5ACA1181	AC095046	GCCTGTGCAATACAGCAAGA	TAGGGTTGTTCACCGTCCTC	60	FP	152	470	AAAAAAAGTAAGAAGG
Ya5ACA1182	AC105413	TCACGCTTTTTAGGTAAGGAAA	GCTCCAGGCACCTAGAAGAG	55	FP	142	459	AGGAACTCTTCTAG
Ya5ACA1183	AC073840	TGATGGAAGTTTCCAGAGGC	GGAGCCTTTAAGCCTTGGTC	60	FP	122	437	AAAAAAAGAACAGTATA
Ya5ACA1184	AC007799	TGGCTCTAATGACCAAAAGGA	CCCAGGTGATTCATTCCATC	55	IF	150	467	AAAAAGAAACAAGATT
Ya5ACA1185	AC079140	CAGCTTAAAGGCTTTTCCACA	CCTTTAGACAGTCCGGAAACC	60	HF	96	378	AAGAATTCTCC
Ya5ACA1186	AC022878	GGGTGTGCACCCTACACTTT	GCCCTGGAGACAGAGAGATG	60	FP	142	458	AAGAGTTAGTTTA
Ya5ACA1187	AC098582	TTCAGCTTTGATGTGTTCGC	CAAGCAATGCAGAAGATTGG	60	FP	643	958	AGAAAAGGATATTCAG
Ya5ACA1189	AC105445	NOT AMPLIFIABLE	NOT AMPLIFIABLE	-	NA	-	-	AAAAATTCCT
Ya5ACA1190	AC105394	TCAGTTGATGAGCACTCAAGATT	ACTCTAATACAGTAATAATGGGGCA	60	FP	177	486	AAGAAATTATACTTTG
Ya5ACA1191	AC006338	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AAAAGATAAATTAGA
Ya5ACA1192	AC097484	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AAAAATTTAGCCGGGC
Ya5ACA1193	AC093862	ACCCCAGAATACTCCCATAC	GGAATTACAGGCATGAGCTA	55	FP	172	493	AAGAAATAGGCAGTA
Ya5ACA1194	AC013762	GAGAGGGTACGAGGTGTGGA	GATAAGTTGGGTCGAGGCAG	60	FP	168	484	AAAAGATCTGAGTGGG
Ya5ACA1195	AC093862	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AAGAATAGATCAA
Ya5ACA1196	AC113152	NOT AMPLIFIABLE	NOT AMPLIFIABLE	-	NA	-	-	AAAAATACACGGCCAG
Ya5ACA1197	AC093778	TCCATAACCTGTTTGCTTTTACC	TGCAAGCCACACAGAAGACT	60	LF	182	498	GAAGAGTT
Ya5ACA1198	AC005699	TAAACCTTTATTGGCCCTGT	TCTCTACCTTATGACTTTGGGTAT	60	FP	195	499	AGTG
Ya5ACA1199	AC104077	CCCACTCATGTCCCTCTTGT	GCGAGTGGACTCAATAAGGG	60	FP	134	453	AAAAACCAACCCTT
Ya5ACA1200	AC083902	TGAGCTTCTCCTGTTTTCCC	ATGCCATTTCCCAATTATGC	60	FP	124	434	AAAAAATTTAA
Ya5ACA1201	AC021878	AGAGTTGCAGGCTCCTGTGT	TGTGTGTGTGGCTTCTGTTG	60	FP	171	479	AAGAACCACTGG
Ya5ACA1202	AP002026	ATCAGCTTTGCCTAAACCTA	GAACCTTTTCTTGGGGTCT	60	LF	184	500	AGAAAGGGGTCTTTTC
Ya5ACA1203	AC004544	NOT AMPLIFIABLE	NOT AMPLIFIABLE	-		-	-	AGAAATGAGAGACTTG
Ya5ACA1204	AC021878	TTCTCATCTAGAAGCAAAGGATGA	TGACCAGAACAAAACTTGCAC	60	HF	110	431	AAAATTATACCCTGCT
Ya5ACA1205	AC020556	ATGCCCTGTAAGTCCCACAT	CCAAATTGGAATCCTATAGCTGA	60	FP	183	499	AAAAGGCCTGTCAC
Ya5ACA1207	AC093786	TCATTTTGGAAATATGTCTGCC	AAAATGGTACAATCTTTTCACCTC	55	FP	200	488	AAATGTTGG
Ya5ACA1208	AC093694	NOT AMPLIFIABLE	NOT AMPLIFIABLE	-	NA	-	-	AGAAATATATAAAAA
Ya5ACA1209	AC098487	NOT AMPLIFIABLE	NOT AMPLIFIABLE	-	NA	-	-	GAAATA
Ya5ACA1210	AC021120	NOT AMPLIFIABLE	NOT AMPLIFIABLE	-	NA	-	-	TAATAATATTACATGG
Ya5ACA1211	AC093789	NOT AMPLIFIABLE	NOT AMPLIFIABLE	-	NA	-	-	AAAAGGCTAACATTT

(table cont.)

Ya5ACA1212	AC073344	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AAAAGGTAATAA
Ya5ACA1213	AC073344	NOT AMPLIFIABLE	NOT AMPLIFIABLE	-	NA	-	-	AATAAGGTCACTTTA
Ya5ACA1214	AL121577	ACAACGTCAGAGACCCCACT	TGCAATTCTTGCTGATGTTTT	60	FP	207	481	ATAAAAATA
Ya5ACA1215	AC106052	ATTGGGGGAAAAGGAAACAG	GCTCACTTAGGCACCTTGAAA	60	FP	160	485	NONE
Ya5ACA1216	AL359699	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	NONE
Ya5ACA1217	AC098798	TTTGCCATTTTCTTGTTTGA	TTTCACCTGGTTCTTTTTGA	60	LF	136	462	AAGAGATAGTGTGAG
Ya5ACA1218	AF254983	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	NONE
Ya5ACA1219	AC112717	ACTTTATTGTGGTGGTCTGG	CACAAGGTAGCAGAACATGA	55	FP	303	545	AAAGTTTGTCTCTCCC
Ya5ACA1220	AC104828	GAAATTGGCTTGATACCCCA	GGAGACCCTGATCATCTTCG	60	FP	155	460	AAGAAATTGATAATACCG
Ya5ACA1221	AP001819	CGTCTCAGACACATGATAGG	CTTGGAAAGACTCAGAAATCA	55	FP	80	398	AAGAGACAACCTCAG
Ya5ACA1222	AC096761	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AAAAGCTCCCTCCG
Ya5ACA1223	AC093868	TTCATGTTATAAAGGCAAAAAGCA	CAAAACATTATTTCCTGGCTTGT	55	FP	131	441	AAAAATGTAAAGGA
Ya5ACA1224	AC105917	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	NONE
Ya5ACA1225	AC024595	CTTCATCTTGCTTGCCTGGT	TTTCATGAATTACTGAAGGTGATTG	60	FP	143	457	AAGAAATACAATCACCT
Ya5ACA1226	AC018696	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AAGAAAAGGATGCCT
Ya5ACA1227	AC105314	TCTCATCACATGGAACAAGCA	GAAGGCAAAAGGTGTGCAAT	60	FP	145	468	AAGACCTACAGAGTTGG
Ya5ACA1228	AC104828	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	CTATC
Ya5ACA1229	AC093876	ACCTCTTCGCTGCATGATTT	CATACATGGAAGCAAGAAACAGA	55	FP	132	412	AAAAAATTTCCTA
Ya5ACA1230	AC093815	TGTGGAAAGAGGCGAATTAT	TGATGCCACTTAGGAATGAA	60	FP	354	666	AAGAATATGACTCTG
Ya5ACA1231	AC097513	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AGGTTATTCTCTCTCATT
Ya5ACA1232	AC097513	NOT AMPLIFIABLE	NOT AMPLIFIABLE	-	NA	-	-	AGAAAATAAAAGACT
Ya5ACA1233	AC024248	CACACACTATCATACCCGAAT	AGCAGTTCAGAACCATCCTA	60	LF	80	398	AAAAATTTT
Ya5ACA1234	AC097513	TTCAATATTTCTCTTCCTGGCAA	AAGATCAGGCCCTGTGACTTA	60	FP	126	440	AAGAAATAAGTTG
Ya5ACA1235	AC096745	CCATTTGCAAGCAGAAAAGA	GAGTCAGCTGGGGACTATGC	60	FP	149	461	TTAAAAGAAAA
Ya5ACA1236	AC108930	NOT AMPLIFIABLE	NOT AMPLIFIABLE	-	NA	-	-	AAAGACTTC
Ya5ACA1237	AC025741	CGGGCATAATAATGGTTGCT	ATGAAGGTGAGGAATGGCTG	60	FP	105	415	AGAAAGTGCTCAGGAG
Ya5ACA1238	AC125245	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	CCTTC
Ya5ACA1239	AC108030	AAATGTTCCCTGCCTGTGAC	GAGCCACCAACATTAGGGAA	60	FP	164	479	AAGAAGGCCC
Ya5ACA1240	AC022489	CCATTGCATGTCTCTCCTCA	CTTCGATCAAGTGCCCATTA	60	FP	169	495	AAAAATTCTAG
Ya5ACA1241	AC104068	TCATTGAGATGTATGCACCA	TGGCCGCTACACTTATTATT	60	FP	179	496	AGGATAAAATGTC
Ya5ACA1242	AC107048	GCGAGGGCCTTATAAAAGATG	ATTGGGTTTCACATCCGTGT	60	LF	151	471	AAAAGATGCTGCAATGA
Ya5ACA1243	AC093807	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AAAAAGTGGGCAAAGG
Ya5ACA1244	AC093825	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AAGAGATTTTTC
Ya5ACA1245	AC097492	TGCCTCTGGGAAATTTGATT	GCCCAATGTTTTGGAATTGT	55	FP	180	499	AGAAATGATCATGCTGG

(table cont.)

Ya5ACA1246	AC016398	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	NONE
Ya5ACA1247	AC093825	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AAAAAGCCAGGCATGG
Ya5ACA1248	AC121154	TGCTGAAATCTGAAGAGTGCC	GCTTCCTTCTCCATCATTGC	60	FP	89	405	AAAAAAAGATCATC
Ya5ACA1249	AC016398	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AAAAAATGATGAGTTC
Ya5ACA1250	AC025038	GACCTGGGCCAAAATGAGTA	TTTCTGAGGAGGAGGAGGAA	60	HF	170	496	NONE
Ya5ACA1251	AC093916	GGCAGATACTGTGAAATGCT	AAGTGCTGGGATTACAGATG	60	HF	170	489	AAGAAAAAGATGGG
Ya5ACA1252	AC015631	CAAATAAAAGGATGTTTGCATGA	CAGAGGTATGGATCTGAAATGC	60	FP	110	419	AAAAAGAAAATGCA
Ya5ACA1253	AC098593	TTTTAAAAAGCAGCAAACACG	TTTTTGAATGTTTAATGCTGTGA	55	FP	178	500	AAAGACCTCAGATTA
Ya5ACA1254	AC097511	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	CCCTTTTA
Ya5ACA1255	AC131182	TTAGCCTACCAAACAAGTCC	GAAAGCTCAGACCTTACCAG	60	FP	160	469	AAAACCATTTTG
Ya5ACA1256	AC048378	CCATGGATTGATGGGAAATAA	TGGGAGGAACAGATGAAAGG	60	FP	183	497	NONE
Ya5ACA1257	AC096729	AAATACCAGTAACGGTGTTGAGC	AATCTTGCTAAATTAAAGCAGAAA	55	IF	155	466	NONE
Ya5ACA1258	AC093905	CAGGGGGTCTAAAAAGGTTTG	GCAGGGTCAAGAAATACAGGA	55	FP	214	492	AAAAAATAATTTC
Ya5ACA1259	AC097475	TTTTGGAATACAGCCCATTTG	GCACATTCCAAGATTAAAGTGG	55	HF	138	451	ATATTTTAAAAG
Ya5ACA1260	AC093796	TAGCAGCATGGATTTTGCAG	GTGTGCTGGACACTGTGCTT	55	FP	179	491	GAATTAAATGAGAATAG
Ya5ACA1261	AC093890	CAACAACCAATATAGCTGTGTCC	TGGAAGATTGAAGGTGATAATGC	60	FP	178	499	ATATAAAATAGT
Ya5ACA1262	AC010683	ATGGTGAATGAGTCCTGCAA	GCAAAGAATTGCCAGGAAAA	55	FP	169	484	AACAATTTCGG
Ya5ACA1263	AC027058	CAGTTGGGCCACCTATCACT	CAATTATACAATTCATGGGGTTAA	55	FP	193	496	AAGAAAATTGATG
Ya5ACA1264	AC093887	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	GAAAAACGGCGCACTA
Ya5ACA1265	AC106879	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	NONE
Ya5ACA1266	AC097465	CATCATGTTGCTTACTTTAAACAT	TTGTTTTGCAATTACTGTGG	55	FP	82	399	AAAACTGACAAATT
Ya5ACA1268	AC110813	END OF SEQUENCING CONTIG	END OF SEQUENCING CONTIG	-	EC	-	-	NONE
Ya5ACA1269	AC020708	CTGTGGAGGGAAGGAGACAG	GGATGATATGGGAGGGGAGT	55	FP	200	491	NONE
Ya5ACA1270	AC104819	GCCAAAGAAGGCTCATGTTG	TCTCCCGCATCATTCCTTAC	60	FP	134	453	AAGTCATCATTAGG
Ya5ACA1271	AC013477	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AGAGAGTCTAG
Ya5ACA1272	AC093700	CTAGCAGCCATGTAGTCGAT	TTTAGTAGAGACGGGGGTTT	60	FP	180	500	AATAATAGTCG
Ya5ACA1273	AC019341	CCAATAAACACGGGTTATTCTCA	TGGCTCAAAAGTAACCTCAGC	60	FP	186	472	AAAATACACATATTT
Ya5ACA1274	AC097507	AAGCCAGATAACCTTCTCGGT	GCTGAGATCAAGAGGCCAAC	60	HF	133	444	AAAGATGAGG
Ya5ACA1275	AC055120	AGCCTTGCTCCGAACAATAA	ATGGCCATTGAGGTCAGCTA	60	FP	128	443	AAAAACCACTTTGGG
Ya5ACA1276	AC093163	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AACAATCAGA
Ya5ACA1277	AC108064	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AAAAATGTAGTTGT
Ya5ACA1278	AC093803	AGTAAAATTTGCGGGTGTGG	GGTGGCTAATTCGATGTGCT	60	FP	627	953	TGTGGGG
Ya5ACA1279	AC093764	ACGCCAACCCTGCTATTGTA	AGCACAGGCTCTGGAAACAT	55	FP	109	417	AAAATACTGAAGCTAG
Ya5ACA1280	AC074255	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	NONE

(table cont.)

Ya5ACA1281	AC074254	CCATGGAAGAGGAGCACTGT	CCACAAATTAAAATATGGGGCT	60	FP	198	498	AAAAATAACTTTT
Ya5ACA1282	AC069302	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	TAAAAAAATGGATCA
Ya5ACA1283	AC093694	TGTCCATAATTCAAAGTCAGGC	TGTGTAATTGTTTCTTAGGCTTTCA	60	FP	174	496	AAAATTAAATATTTG
Ya5ACA1284	AC096723	AGTGAGAAAGAATGATGCCCA	TTCATTCCGACATTCCACAA	60	FP	117	434	AAAGAATGATGCCCAG
Ya5ACA1286	AC093801	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AAAAAACGGC
Ya5ACA1287	AC097653	CATGTTACCTTCCTTTCCATTTTC	GATTGGCTGGTCTGTGCT	55	FP	192	500	AAAAATCAT
Ya5ACA1288	AC097518	GGGGCCTCCTACCTATAGCA	ATGAACCCAGGGATGAAATG	55	FP	145	454	AAGCACTGTG
Ya5ACA1289	AC096567	TGTAAGCTTTTTAGAATGCAGGC	AAAGCCAACTAAACTCTGCTCA	60	FP	183	491	ATCTAAACA
Ya5ACA1290	AC093689	AGACTGTGGTTTGGCATGTG	TGAACAGGCCATTCCTTTC	60	FP	126	460	GAAAGGAATGGCCTG
Ya5ACA1291	AC004053	AAAAACACCAATGCTTCAATG	TGACCTTTATCACATTTCCTTGG	55	FP	130	427	AGAAAAAGCTGATTAGT
CHROMOSOME 5								
Ya5NBC15	AC008676	CTTTCCTCAGCTTGGTTTATTCTACTG	GAAGATTCAGGTGGACAGAAAAAC	60	FP	192	502	GTGAAATTCTT
Ya5NBC16	AC008608	CTTAACCAAAATAGTGGACGAGGTT	CAGAAGTATTTACTACTCGAACAG	65	HF	229	539	TGGAACAGTCTT
Ya5NBC18	AC008433	AGACCATCTTTAAGAGGAATACCATGT	GAAACGTAAATTTGTTAATAAAGTGGTGAC	65	HF	180	495	AGAAATGAAGCTC
Ya5NBC21	AC008482	AGCTGTCGTTCAAATGAGACTTTCT	AAGCTCACTCATCAATAAGAACACC	60	FP	177	512	AGAAATTCTTTAATTTT
Ya5NBC25	AC004220	GTGAAGGACATGAACAGACACTTCT	CACCAACAGTGTAAAAGTGTTCCTA	55	FP	218	538	AAAAAGTCAGGAAAC
Ya5NBC40	AC008887	ATTGATCTCCAACTGATGCCCTA	GACAACAGACTTACCCTGCCTATAC	58	FP	105	417	GAATTG
Ya5NBC41	AC008828	CTCTTTATGGGACTTGACAAGCA	GTTCTACATTGCCATAATAGTGTAG	55	FP	128	441	NONE
Ya5NBC58	AC008376	TGCCTCTTTAACCAATTTCTCTTATTTTC	TATTTGGCTGGATTTGAGTTATCTC	60	FP	141	481	NONE
Ya5NBC82	AC005217	AGTGCTGGGAAGACCAGT	GCTGGTGCTCTTGACAAA	60	FP	37	348	GACCAGTCTTT
Ya5NBC94	AC008788	ATTGTCTTTCCTGTGCTACTCTCAT	CACTTTAGTGGATGCTTATCTTTG	57	FP	201	531	CCTCATTTTCTCTT
Ya5NBC110	AC004761	GAGTCTTTGTTCTGTTAACTTAGTGGTGAG	CTAGAAGGTCACACATATGTCAAGG	60	FP	170	558	GGCTTGGACCTTCTT
Ya5NBC123	AC005739	ATCAAGTTGACACTCAGTATTCACCAC	CTAGTCTGCAGAACTGTGAGAAAT	55	IF	180	490	AGAACAAAATACT
Ya5NBC130	AC004629	GTTGTGTCCACTCTTTGACTAGTATGA	GACAGTTTTACTGACTACACAGGAT	60	FP	287	602	ACTTGACTTGATTT
Ya5NBC311	AC008843	TCTTGGCAAGGAGATGTGAA	AATCACATCCGAGGGTGTCT	60	IF	279	584	AAACTGGTGTTCC
Ya5 440	AC005754	TCTGAAGGAGGGAACCAAGA	TGCTTCAAGGTAAAAGTGGT	60	FP	124	439	AAAATAGGACTGG
Ya5 456	AC004038	GGTAACAAAGCCCCTGCATA	CAAGCTTCACAAACCAATGTTC	58	FP	197	510	CTAGACAGCTTTT
Ya5 472	U67231	CAGCTAAAGAGATCCCACGTT	GGAATCATGTGAGACTGAATTGG	55	FP	105	430	AGAAGCACCCCACTCCC
Ya5 474	U67229	AGGGAGTGGTAGTGGTTGGA	TGAATCAAGTTATGTGACTCT	55	FP	179	503	AGAAATAATTTAGTG
Ya5 513	AC016576	TGGCAGGTAGAGTAGCCAAAA	GGCTGTGTAGGAGGTGAGACA	58	LF	139	436	AAAAGAAGAC
Ya5 517	AC008795	GCACACATTTCAAGCCAGTG	GAGTGTTAGAACAGTCGTGTACATT	60	FP	117	433	AAAATTACTTTC
Ya5 529	AC008716	TTCCCTCTTCCTGAAGCAAA	GATTAGGGGCCTTCCATAGG	55	FP	116	431	AAACATAAAGATTCTGG
Ya5NBC1	L43392	GGAATAGGAGATCCAGTAACTTC	GTAGTGTTCAGAGACAGCACTTTA	55	HF	185	544	AACTTCT

(table cont.)

Ya5ACA1292	AC016603	AACCAATGCTGGGGTTATTAAG	TGCCCAGTTGAGTTCAGAAA	60	LF	169	499	GATTTAG
Ya5ACA1293	AC008601	TCAACATCTTGGCAGTGCTC	ATCTAAGGCTTTGGGTCCGT	55	FP	152	469	AAAACACCATATAC
Ya5ACA1294	AC116345	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AAAACAACAGACAT
Ya5ACA1295	AC016585	GGGTCTAAAACATTTGCTTG	CAGAGGGTTCTTGATTCTTG	55	FP	~260	639	NONE
Ya5ACA1296	AC090063	TACCACCTCTGAAACCCTTC	GTTGGGATGGATTACAGTCA	55	FP	105	421	AAGAAGGCCAGAAGG
Ya5ACA1297	AC008610	AGTACAGCTAAGCAGGCCCA	ACCATCCAATCCCACTCAAA	55	FP	130	438	AAAAACCTTTCCAG
Ya5ACA1298	AC113423	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	ACAAA
Ya5ACA1300	AC117528	NOT AMPLIFIABLE	NOT AMPLIFIABLE	-	NA	-	-	AAAAGTTTA
Ya5ACA1301	AC034247	CTCACCAGGTTTGGTGTGTG	ATCTTTGTCCCCGGTCTCTT	55	FP	435	734	AAAAAAAGATTCC
Ya5ACA1302	AC104117	TGTCATAGAAAAACGGGCAA	CCCTGCCCAAATTTGAAAC	55	FP	190	498	AAGATGTTCAACCTC
Ya5ACA1303	AC008514	GAAATCTTAAGCAGCCACTCAAA	ACTCTGTGGATTCACCAGGC	55	FP	83	398	AAAAGGAAAAAAAG
Ya5ACA1304	AC008665	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AAAGAG
Ya5ACA1305	AC027333	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AAGAGACTAAG
Ya5ACA1306	AC008562	AGGCTTAATTTCGGGGTACG	TTTCCAATGAATGTTATATGTGATG	55	FP	150	473	AAAAAATAACATCAC
Ya5ACA1307	AC022439	TAAGGGGGTCATGAACTTGC	TGCTCATATTTCCCCTGAGC	55	FP	149	461	AAGAAGCAAGACAG
Ya5ACA1308	AC010603	CCTGAACAAGGCTAGGCAAG	CGGGCCAAGTTTGATTCTTA	55	FP	577	892	NONE
Ya5ACA1309	AC091931	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AAAAATAACATTGGACA
Ya5ACA1310	AC016574	TTGCTTCTTAGCATGTTGTG	CAAAGTGTTGGGGATTACAG	55	FP	127	442	AAAAAATTTTCC
Ya5ACA1311	AC026736	TGCTTGGTGATGAAGTGTCA	AAGCGTTCTAGACTTCAGCTATTTT	55	FP	165	493	NONE
Ya5ACA1312	AC093264	GCCATCAGAGAAATGCAAAT	CTAGTTTTCATCTTCACCATTTTT	55	FP	130	400	AATTAAT
Ya5ACA1313	AC025457	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AAAAAGTTTAAGTTCT
Ya5ACA1314	AC034222	CTTCCTTGCCATCTTTGCTC	TGTGGTGAACCTCCTTGTTTT	55	FP	485	805	AAAAGATGGGTA
Ya5ACA1315	AC01863	GCAAAGGAGCTGTATGGACAA	TGCTGTTGCATGAATCTCAA	55	FP	142	449	ATGTGG
Ya5ACA1316	AC109474	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	NONE
Ya5ACA1317	AC026798	AAAGCTCTTCACTGCCCAAA	AAAACGTGCAATCTCAACCC	55	FP	193	493	AAAAAGTAAAGGTTGG
Ya5ACA1318	AC109455	AAATCATGAAGAAGAACAAAGT	TGTTGGCCATTTATATGTCTT	55	HF	81	400	AAGATAAAAAATCTG
Ya5ACA1319	AC091828	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AAGAAAACTGAGGCA
Ya5ACA1320	AC091946	TGCCCTTGTATTCTTACAGCC	GATTGGTGGCTCCATCATGT	55	IF	156	479	AAAAAAAATTATTTT
Ya5ACA1321	AC091946	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AAGAAATAAGTTCAT
Ya5ACA1322	AC011389	NOT AMPLIFIABLE	NOT AMPLIFIABLE	-	NA	-	-	NONE
Ya5ACA1323	AC008435	TCCTTCCCTCAAAGCTCAAA	TCAAAGGACACCCATAGCACT	55	FP	123	430	AAAAAATAGT
Ya5ACA1324	AC114323	NOT AMPLIFIABLE	NOT AMPLIFIABLE	-	NA	-	-	NONE
Ya5ACA1325	AC016620	TTCTCCCCCAAGTTGAGCTA	GCTAGTTTTGGCCCTTTGTG	55	FP	120	433	AAAATTTACATGGAAG
Ya5ACA1326	AC092354	NOT AMPLIFIABLE	NOT AMPLIFIABLE	-	NA	-	-	AAACAAATAAAAACTC

(table cont.)

Ya5ACA1327	AC090071	AGGTCTAGCCGTGCCACTAA	CCTATGGCACCTCAGCTGTT	55	FP	104	449	AAAACAAGACAACT
Ya5ACA1328	AC008961	CTGGGCAAGCCAGATTTTAG	AGAAAGCTTTTCTGTTGATTGG	60	FP	197	500	AGAAAAAAATGCTTGA
Ya5ACA1330	AC139500	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AAGATTTAGGAGTTG
Ya5ACA1331	AC010165	NOT AMPLIFIABLE	NOT AMPLIFIABLE	-	NA	-	-	AAAAGAGTATAATTGG
Ya5ACA1332	AC116363	TTAGTACTCCTGGGGAAAGG	CCACGGCTTTGTTTGAGAT	60	FP	272	590	AGAATATTCCATAGTC
Ya5ACA1334	AC025170	ATTTCTGGGCCAAGGAGTTT	GCACTCTGTGTGTGGCTTGT	60	FP	695	939	AAAAATAATTAAAATGA
Ya5ACA1335	AC025755	GGCATGGAAACTAGAGGAAC	AAGTGATTCTCCTGCCTCAG	60	LF	287	597	AAGAGATCGAGACC
Ya5ACA1336	AC114963	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AAAAATTACAGTTTTA
Ya5ACA1337	AC108120	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AAAAATCAG
Ya5ACA1338	AC093214	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AAAAGACAAGGA
Ya5ACA1339	AC026697	CAGCCACAACAAAGCAAGAA	TATTTATGCAGGGCCTTGGT	60	LF	132	450	AAACAGAATAA
Ya5ACA1340	AC008897	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	140	451	AAAATTAATTTTT
Ya5ACA1342	AC011341	TGTGTGTGTATGTGCATGGC	CCTGATTCATTCGTGCCTTT	55	FP	515	826	AGACGT
Ya5ACA1343	AC008434	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AAGATGGACTAAAGA
Ya5ACA1344	AC106800	NOT AMPLIFIABLE	NOT AMPLIFIABLE	-	NA	-	-	AAAAGGCTAGCG
Ya5ACA1347	AC069033	CTGAGGAACTGGAGAGCAGG	TGTGCAATTCAGTAGCTGGG	60	FP	559	869	AAAATAAATGTCAT
Ya5ACA1348	AC114969	NOT AMPLIFIABLE	NOT AMPLIFIABLE	-	NA	-	-	NONE
Ya5ACA1349	AC091866	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AAAACTACATATTA
Ya5ACA1350	AC109492	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AAAGAAAATATTT
Ya5ACA1351	AC025466	CTGGCATGTTAGTGGCACAT	TGGGAATTTGTGTCTCCTAGC	60	FP	176	492	AACAATCATGATG
Ya5ACA1352	AC020921	TTGGGGAAATTGCTCTGTTC	AATGCTGGATGAAGAGCAGG	55	IF	157	476	AGAATCCTCCAGTCAG
Ya5ACA1353	AC026782	ACATGGTCCCAAGGAAAACA	CCCTGAGGTCATTGTGCAT	55	FP	151	471	AAAGAAAGGAGAAAGGTT
Ya5ACA1354	AC023134	TCCATACCTCATTTGTCGCA	GAAACAGCTTTGCAGGTCGT	55	FP	134	441	AAAACCTAACCT
Ya5ACA1355	AC008525	GGGTGGTCACAAAGACCAAG	TAGGCCATGTTTTCCTCCAC	55	IF	163	500	AAAAGTAGTAAAAAA
Ya5ACA1356	AC093510	GGTCCCAACTGCCAATAAAA	TGCATCACTGGGACATAAAA	55	FP	164	487	AAAAATCACAATTTTT
Ya5ACA1357	AC008873	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AAAAATTAACCTTGC
Ya5ACA1358	AC113423	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AAAAGAGGATACAAA
Ya5ACA1359	AC010306	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AGAAAATCATACCAGTG
Ya5ACA1360	AC025175	GCAAACTGGCCAGAAATCAT	ACAGAAGATGGTGGTGGAGG	60	LF	132	437	AAAACCAGCTCCC
Ya5ACA1361	AC008391	CTAAGCAACCACTCATCTGC	ATGCATCAAAGGAAGACCTG	55	FP	211	485	AAGCAGAACC
Ya5ACA1362	AC010455	TGCATCATAAAATGTGCTGTCA	CCCAATTGCCTTTTTCTTCA	55	FP	127	448	AATAAATGTCGGCA
Ya5ACA1363	AC008378	TAGCCTACCCCACAGAGGTG	GGCAAATGTGGATGGAATCT	60	FP	137	450	AAGAATGATTTTACAG
Ya5ACA1365	AC116357	NOT AMPLIFIABLE	NOT AMPLIFIABLE	-	NA	-	-	AAAAAGCTTTAGAG
Ya5ACA1366	AC010633	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AAGAATTCCAG

(table cont.)

Ya5ACA1367	AC010285	GTCAGTCCTGTGCCTTGTTG	TACAAGACGGGCTGTGTGAG	60	FP	162	470	AAAGAATTTTGAATTT
Ya5ACA1368	AC008519	TGTCAGAGGCTAACAAAATGA	GACACAGTGTTCACATCTATCTCT	60	IF	178	498	AAAATGTGTGTGTG
Ya5ACA1369	AC091851	NOT AMPLIFIABLE	NOT AMPLIFIABLE	-	NA	-	-	GAAAATAACACATCTG
Ya5ACA1370	AC011389	TCATCTTTTCTGCCAGCCTT	CTAAGCTGCCTTGCATTCCT	60	HF	183	496	AAAGATTTGAGATGG
Ya5ACA1371	AC012612	TGAAGAGCAGAAAGGCTTCA	AGCCCTGTTGTTAATCCCCT	60	FP	98	449	AAAAGATAGTATTTGAG
Ya5ACA1372	AL009030	TCATTGCCTCTAAAAAGTTGTG	TGCCTTTAAGCAACAAAACA	60	FP	282	597	AAAAGATTTAGTTA
Ya5ACA1373	AC008948	NOT AMPLIFIABLE	NOT AMPLIFIABLE	-	NA	-	-	AAAAAACCGAAAAGCT
Ya5ACA1374	AC008501	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AAGAATGTTGA
Ya5ACA1375	AC008462	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AAAAAATGGGAT
Ya5ACA1376	AC011366	TTTCAGTCTTGGACCATTTCAG	TCTTCGACTCATGTTAGGCAC	60	HF	154	472	AGAAAGTGCCTAACATG
Ya5ACA1377	AC010625	GCAGGGAGGGAGGTTAAATC	CCAAATTTTGTGACTTCAGGG	55	FP	178	488	AAAAATTTCAGTGTC
Ya5ACA1378	AC010431	CACCAGGCTCCAACCTGTAT	AAAACCTAGCAGGGCAGACA	55	FP	179	494	AAAAAAGATTATTC
Ya5ACA1379	AC012610	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AAAATGACAATTGA
Ya5ACA1380	AC025182	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AAAGGTAGAAGGAGCCC
Ya5ACA1381	AC010276	TTCAGCATGGAGTATAAAACATAG	TGAGCGTACAGTCACCATGA	55	FP	187	493	AAAACATAG
Ya5ACA1382	AC010355	NOT AMPLIFIABLE	NOT AMPLIFIABLE	-	NA	-	-	AAAAATGAAC
Ya5ACA1383	AC104110	NOT AMPLIFIABLE	NOT AMPLIFIABLE	-	NA	-	-	NONE
Ya5ACA1384	AC008693	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AGACAAAG
Ya5ACA1385	AC113418	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	NONE
Ya5ACA1386	AC106806	CTAGTCCTCCCTCCCTGGAT	TGCATGGCAGTATCATTGCT	55	FP	686	994	AAAGAGTGAGACCTTG
Ya5ACA1389	AC093278	GACTGGGATGCTTTTGAAAC	TCTGAAAGGTGGAATTTGACT	60	FP	264	587	AATAATTTCATTAATC
Ya5ACA1391	AC004041	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AAAAAAAAGAATTC
Ya5ACA1392	AC026398	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	NONE
Ya5ACA1394	BC013423	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AAGATTTCAACATATG
Ya5ACA1395	AC011409	TGCAGTTTAAAAATTGGAAAAGG	TGCACTCTGGGAAACATAAACA	55	FP	185	498	AAAAATTGGAAAAGGAG
Ya5ACA1400	AC109454	AAACTGAAAATGCAGGTGCC	TTCCTCTGAAAGGCTGGAAA	60	HF	379	677	CCTAAGT
Ya5ACA1401	AC097492	CACGCTAACCAAAGAATCAACA	ATCTTTTGCCCCATGTTTTG	55	FP	164	487	AGAAATGATCATGCTGG
Ya5ACA1402	AC034243	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AATTA
Ya5ACA1403	AC008614	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AAGAGTCATCACC
Ya5ACA1405	AC034243	ATACCTGTGGCATCCTGTCC	CCAACCAACGATAGAAAGATCA	55	FP	130	452	AAAATTATGTAACTTG
Ya5ACA1406	AC008716	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AGACGT
Ya5ACA1407	AC122706	NOT AMPLIFIABLE	NOT AMPLIFIABLE	-	NA	-	-	AAGACTGTTCCA
Ya5ACA1408	AC008533	NOT AMPLIFIABLE	NOT AMPLIFIABLE	-	NA	-	-	AAAAATAGACAGACAG
Ya5ACA1410	AC016598	ACCAAGCCTCCTTCTATGGT	CTCCTTTTCCTGCTGCATGT	55	IF	169	481	AAAAATAAAAGTAT

(table cont.)

Ya5ACA1411	AC010489	NOT AMPLIFIABLE	NOT AMPLIFIABLE	-	NA			AAGACCACGTGA
Ya5ACA1412	AC025755	GAAACGAGGGGATGAGAACA	GGGGGTGGGAGGTAAAGATA	55	FP	140	489	AAACAT
Ya5ACA1413	AC005216	GCCCTGATAAGAATAGGAGGC	TTTGAATCATAACTGTTGCTTTCA	55	FP	164	476	AAAAGACCTTTC
Ya5ACA1414	AC022099	CAAAAATGGGAAAGTGATCC	CATGAGTTTTGGAGTGGACA	55	FP	101	422	AAGAATAAACAGGTTTT
Ya5ACA1415	AC091991	GAATGGGAAGACTTGGTGTC	AGGTCATGGATAGGCTTCAG	55	FP	278	594	AAAAATGAACATAAATG
Ya5ACA1416	AC008571	NOT AMPLIFIABLE	NOT AMPLIFIABLE	-	NA	-	-	AAAAAATACATTTAAG
Ya5ACA1417	AC112169	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	NONE
Ya5ACA1418	AC011368	NOT AMPLIFIABLE	NOT AMPLIFIABLE	-	NA	-	-	AAAGAAAATTC
Ya5ACA1419	AC131565	TGGTAGTTCCTTGGGACCTG	TGATTTTGTGGAGGAGAGAGG	60	FP	104	425	AAAAGCAGACACTA
Ya5ACA1420	AC011409	NOT AMPLIFIABLE	NOT AMPLIFIABLE	-	NA	-	-	AAAAATTGGAAAAGGAG
Ya5ACA1422	AC008694	GCAAATTTCCTGAGGCAGAG	TAAAATGCAGATTTTGGCCC	55	FP	115	435	AAAGAGGTAGTGCAG
Ya5ACA1424	AC008685	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AAAAAAAGACATCTTGG
Ya5ACA1425	AC011344	NOT AMPLIFIABLE	NOT AMPLIFIABLE	-	NA	-	-	AAAAACAGGAGG
Ya5ACA1426	AC067762	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AAAAAAGAAATCT
Ya5ACA1427	AC091884	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	CTCTAGGCCAG
Ya5ACA1428	AC008658	NOT AMPLIFIABLE	NOT AMPLIFIABLE	-	NA	-	-	AAGAAGAACAGTCTA
Ya5ACA1429	AC091928	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	ATATATATTATA
Ya5ACA1430	AC122720	NOT AMPLIFIABLE	NOT AMPLIFIABLE	-	NA	-	-	NONE
Ya5ACA1432	AC008607	CATTGTCCTGCATTGGTATCC	TCGGAAATTGTCGACACAGA	60	FP	183	496	TATTTT
Ya5ACA1433	AC091819	AGATTGCTGTTGGACAGCCT	AGCTGCTTGCACACACATTC	55	FP	293	623	AAGAAAGTGATC
Ya5ACA1434	AC114321	CACTGTTGCTTTCTGGCAAA	GAGCCCGAATGCTGTAATGT	55	FP	173	490	AAAAGTAACTTTGCAG
Ya5ACA1435	AC008662	GGTTGATCAAATACAAAATGCG	TTTCCCCTGGAGTCATTGAG	55	FP	86	431	AAAGATGGGACTC
Ya5ACA1436	AC091907	GCATGGAATCAGGACAAGTA	TCACATGGTGAAAGGTGCTA	55	LF	288	598	AAAAAGACCTTAGA
Ya5ACA1437	AC022089	GGTTTGAGTTTAAAGAAATCAGGG	AGGGGACTTCTTTTTGGCAT	55	FP	176	492	AAGACACAAGTGG
Ya5ACA1438	AC008906	CTTGCCTTGGTGCAAGATTT	CAAGGGAAACCGAAACAAGA	60	FP	159	474	AAAAATACTACCAGGATG
Ya5ACA1439	AC022104	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	TCTTTTC

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Ya5NBC3	AL023807	ACTGCTTGAAGCTAGAACTTAAGAGACC	CTCTTGTCTGCTTCTAGACTTGTGA	60	FP	243	564	NONE
Ya5NBC6	AC006344	GATTACATCCTGTGATCCTGAAACT	GAACATTTGTTCTTTTGTGACTGCT	60	FP	189	539	AAGGAAATCAACTTTAA
Ya5NBC43	AL096867	CCTTTCCTTACTAGACAGTGACAACAT	CTTTTAGCCATCTTCTTGGTGTTTG	55	FP	218	539	CATATATGATATCTT
Ya5NBC54	AL024507	GTTTATGTCAGTAGGAGTTTTCTCGTGTAG	TCATTGTATCATCTGCTGTACCTGT	60	LF	130	433	TAGATTTTT
Ya5NBC72	HS234H5	CCTTGCTGCATAAAAACCTA	TATGACTAATGTGGGGCTTT	52	FP	102	416	AAAAACCTAATTGTTTT
Ya5NBC125	AC004206	AGTATTTTGCACTTCTCTAAGGGTGTC	CTGGTCTTATGTTTCATCTGGATTC	60	FP	223	507	CCCAG

(table cont.)

Ya5NBC132	U91328	CTCGTGATTCACAGAAGTGTTGTAAG	CGGGGTTCATCCTTAATACATACAT	60	IF	228	458	TTATAAAGACTTTTT
Ya5NBC161	AL031978	CCTGTCTAAACTCCAGAATGAAGAA	GCAGTAGAAAGATCACAGGCTCTA	60	FP	199	491	AGAATTTT
Ya5NBC171	AL035688	TCTAGAATTACAAGTGCAAGCCATC	CTTCTCATCCCTGCTAACATAACAT	55	LF	130	451	CTCAAAATGTATTTCTT
Ya5NBC186	AL035445	CATCTTCTGAACCCATAGGGAAAAT	GCCAATTGCCTGGTATGTTTTA	55	FP	381	649	AAAAAGCAAA
Ya5NBC192	AC005678	CACTCAGATAAAGATGTGGACTTCA	GCTTTAGAGAGTCTGACTTTGCTTC	60	FP	238	536	ATGCCTG
Ya5NBC196	AL031785	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AGAATAATGGGCTCCA
Ya5NBC197	AL031785b	CAGAAGTAAGATTGCTGGATCGTAT	CTCAATGAGATATCACCTCACACAT	60	LF	204	461	GAAAATAGCC
Ya5NBC215	AL096710	GCCAATCTAAACGAATAATCA	AGGCAGAATGTAGTTGTTGG	60	FP	467	780	NONE
Ya5NBC308	AL133404	CAACAGAGAAGAAATGATCAGTGG	TGGGCCCTATATTTGAACAGA	60	FP	147	429	TACCACTGATTTCTT
Ya5NBC327	AL132799	AGGCAGGTTCAATGTTCAAA	TTGTCTTATTGTGCTGGCTAGA	60	IF	339	668	CTCATTATTCTT
Ya5NBC342	AL049823	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AAAAAATTCTG
Ya5NBC360	AL031121	GAAACAAACATTTGGTAATGATGC	GACCAATGTCACTTATGAAATCCTT	60	FP	61	407	ATTCT
Ya5 426[2]	Z84485	CCACAGTTGGGAGGAATGTT	TTCCCATTTTCCAAGCAAAC	60	FP	97	408	GATACTTTT
Ya5 434	Z99495	TGATCATGACCTTCGTTGGA	GTCTCTGGGCCTCCAAATCT	60	HF	133	455	AAGAAGTCATGCTGG
Ya5 436	AL031577	AGGGGAAATGAAACATGCAC	ACCTTAGGCACCCCTCCTC	60	FP	103	587	NONE
Ya5 437	AL031904	CCACAGTTGGGAGGAATGTT	TTCCCATTTTCCAAGCAAAC	60	FP	178	501	AGAAGTTGAATTTC
Ya5 443	AL031178	TTGCTTCAGAGGATGGGAAT	CAAACGATTCAAGCACAAGG	60	FP	249	582	AGAAATATGTGGTAAT
Ya5 458	AL008627	GTGGCTTAGAGGCGATGTTT	ACCTGGACATGGCCGATTA	60	FP	108	426	GGGAGTATTTTT
Ya5 483	U67216	TCTTGGCTCCAAGTGACAAA	AGCTGCTGAACCAACACTAGC	55	FP	116	397	AACTCAACTACA
Ya5 484	U67215	TCTTGGCTCCAAGTGACAAA	AGCTGCTGAACCAACACTAGC	55	FP	132	397	AAGATTCCC
Ya5 543	AL034372	GATGCAAGTGGACTGAAGCA	TGGATAAAATTGTCCCCACA	55	FP	136	448	AAAAGTCAGTGACATT
Ya5 547[2]	AL360227	TGCATTTGAGAGCACCTGTC	TGTTCCAAAATTCTATGAGGTTTC	60	FP	257	556	NONE
Ya5 557[2]	AL136081	TAAAAGAGGCGCAACGGAGT	TACATGGCACCTTTTTGCTG	60	LF	71	394	NONE
Ya5 569[2]	AL139388	AGGAGATACACTGCGGAGTCA	GGGAAAAGCAACAGAGATGG	60	FP	102	420	AAGAAGAGCTCTGG
Ya5 570[2]	AL139388	TTGCCAGCCTGATGAATATG	AAGCTCTGTTTCCATTGAACATT	60	FP	91	408	AAAAGTATTAACAA
Ya5ACA1440	AL135903	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AAGGGTGGGTCCC
Ya5ACA1441	AL160403	CAAATGCAATTGGAGTGTTCA	ATTGGGCTAAGCACAGGATG	60	HF	541	849	AAAAAGTACTTTTA
Ya5ACA1442	AL513164	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	ACAAAAGATGAAACTC
Ya5ACA1443	AL138832	AAGAGGTGCTAGTAATCACATGG	TTTTGCCCTGCCAATAATTC	55	FP	184	500	AAAAATAAAAATGCA
Ya5ACA1444	AL050340	CATCACTTGGTCAAAATGCCT	TGAAAGCTAGACCAAATCCTGG	60	FP	142	457	AAGATTTGTGTC
Ya5ACA1445	AL512510	TGGATCTAACGGGAAGAAAAA	CGTGAAATGTGAAGACCACC	60	FP	154	468	AAAATTTGGAGAA
Ya5ACA1446	AL450339	AAACTTTTAAAGGCGGCACA	TACTTTCCATGGGGATCAGG	60	FP	28	347	AAAGGCGGCACA
Ya5ACA1450	AL356421	CTGGGTTCTTTTCATGTCAGG	TTCAAAGGAAATTTAACAGGGA	55	FP	126	452	AAGATATATATATATA
Ya5ACA1451	AL359646	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AGAAATATAGCTTCTA

(table cont.)

Ya5ACA1452	AL590553	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AAAGAAATTCAG
Ya5ACA1453	AL590608	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AAGAAAGGGAACATC
Ya5ACA1454	AL009029	GGAGCCAAGGTCACTCATGT	TCGCTGCTTGGAAACTTCTT	55	FP	133	471	AAGAGGGATGATCTA
Ya5ACA1455	AP002529	TGGCAGGAGTTTATATCAGAA	TGTTTTCCTCCAACTCTCAT	55	FP	68	390	AAAGAAACAAAAAC
Ya5ACA1457	AL139191	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	GAAAAACGGACAA
Ya5ACA1458	AL356775	ACAGGCCCATAAAAACATGG	TTGCTTGACTGTTGTGACAGG	60	LF	139	474	AAAAACATGGATTTGG
Ya5ACA1460	AL513547	GAGTCACACTGTGGAAAAGCC	GGATTTCCTACAGTGGGACT	60	FP	145	487	AGAAAATCCTAG
Ya5ACA1461	AL158033	CCCAGCAGTAAAAACTCACCA	CATGGGGTCTTCTGGGACTA	55	FP	118	438	AAGATGAATGAATCTTA
Ya5ACA1462	AF418272	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AAGACTGACACTGTG
Ya5ACA1463	AL445189	TCACTTCCTTCTTAGCACCCTC	GCATTGCCCTGATGAAGTTT	55	FP	148	482	AAAAAACAGTGGTT
Ya5ACA1464	AL121957	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AAAAGATACAGA
Ya5ACA1465	AL109920	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AAGACAGAGTCTC
Ya5ACA1466	Z97206	GTGGAGGGGGAAAAAGAAAT	TTGTGCAGGGAGCTTTAGGT	60	FP	125	449	AGAAATATAAATCATG
Ya5ACA1467	AL513472	ATGTGGGGAATGTTTGGGTA	TCCCCCAACTATTTTCATGC	60	HF	700	1011	AAAAAAAAAAGAGA
Ya5ACA1468	AL136306	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	ATTGGAAAAAC
Ya5ACA1469	AL358942	CCAATGTATTTTTCGGTCATCA	TGCCACAATGCAAATGTTTT	55	FP	169	495	AGAAAGTAGTACA
Ya5ACA1471	AL158035	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AAAGATGACAACAATAG
Ya5ACA1472	AL512427	GGGACTTCTAGCCAGGCTCT	AACTGTGCAACTGCGTCAAG	55	FP	98	406	AAACGTGTGTGATAA
Ya5ACA1473	AL671966	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	NONE
Ya5ACA1474	AL353624	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AAAATATTTTTTTGTG
Ya5ACA1475	AL357141	AGCTTCAGGGTTAGGCCATT	GGTACATCCATTTTAAGGCCA	55	FP	163	479	TGGCCTT
Ya5ACA1476	AL136478	TCAGTTCCAATTCCAGCTCC	CTAATGTTTATGTGTTTTGAAAGG	55	FP	132	445	AAAAATGGGGATAAGG
Ya5ACA1477	Z98172	TGTCCTTGCTGCATAAAAACC	TTGGAATGTAAGGGCCAAAA	55	FP	183	497	AAAAACCTAATTGTT
Ya5ACA1479	AL596219	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	GAAAATGGACATACTG
Ya5ACA1480	AL022722	TCTGTAGCAAAGCACATGAC	GGTTCAAGCAATTCTCCTG	60	HF	346	677	AAAAAAATTAG
Ya5ACA1481	AL049613	TCCTTTCAGGTAAAAGTGGCA	GGTGCTATTGCAGCATTTGA	55	FP	99	415	AAAGTGGCAACAAGGT
Ya5ACA1482	AC020559	TCCCCACCTTCTTCTGAATTA	TCAAAACTCACTGCAGATACCAA	55	FP	77	403	AAAGGAATG
Ya5ACA1483	AL356605	ATGCCTTATGGACATGGGAA	TGAACTCCACTGCTTGTGCT	55	FP	160	446	AAAAATTTC
Ya5ACA1484	AL356278	NOT AMPLIFIABLE	NOT AMPLIFIABLE	-	NA	-	-	AAAAAAGATCTTT
Ya5ACA1485	AL450347	NOT AMPLIFIABLE	NOT AMPLIFIABLE	-	NA	-	-	AGAAAATGTACCTCCTT
Ya5ACA1486	AL356432	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AAAACTCATTCTA
Ya5ACA1488	AL606923	NOT AMPLIFIABLE	NOT AMPLIFIABLE	-	NA	-	-	AAAAATTGACAGATTA
Ya5ACA1489	AL358943	NOT AMPLIFIABLE	NOT AMPLIFIABLE	-	NA	-	-	AAGTATTGTTAAATCACC
Ya5ACA1490	AL121575	NOT AMPLIFIABLE	NOT AMPLIFIABLE	-	NA	-	-	AGAAAGCACATTTTT

(table cont.)

Ya5ACA1491	AL035671	TTCCATTAAGTCAGGCACAAA	CCTGCAACTCCTACCCAGAA	60	LF	143	455	AAAAGTCTTTAGAGTG
Ya5ACA1492	AC010942	GGGAGATTGGTGGGGAATAA	GGTGGTGTGGCTAGGAAAGA	55	IF	123	437	GAAAGTGTATAATTTC
Ya5ACA1493	AL583853	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	ACCTGAG
Ya5ACA1494	AL669984	AAACCAGAGTGGTGCATATCCT	GCTACATCTGTACTTCTGCCCC	60	FP	116	428	AAAATAACATATTTT
Ya5ACA1495	AL355881	AGGCTTTCTGGTGGAAGTGA	GCCTCTCCTTTTTGGAGCTT	55	FP	170	459	AAAAGCTGAGTTA
Ya5ACA1496	AL121959	CATTTGATGGAATACCGATGG	CAGTATCTTTGGGGCATGGT	55	FP	106	416	AAAAAATGA
Ya5ACA1497	AL078590	GCAAGACTTCCTGAAAGGGA	TGCAGTTCCAGAAAAGAGCA	55	LF	142	459	GAAACAGCAGTGGAGG
Ya5ACA1498	AL135839	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	NONE
Ya5ACA1499	AL391595	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AAATAAACTTTA
Ya5ACA1500	AL449363	GCTCTTGGGCAAGTCTGTCT	TCTCTCTACCAATAGGTCCCTCTA	55	FP	145	462	AAAAAATTTTTGTTTTC
Ya5ACA1501	AL512290	CCATTTGGCATAGCTGTTCT	TGCCTGAGTGAGGGTTCTTT	55	FP	160	474	NONE
Ya5ACA1502	AL591499	NOT AMPLIFIABLE	NOT AMPLIFIABLE	-	NA	-	-	AAAAAAAAGTTG
Ya5ACA1503	AL583856	CTGGAAGTTCTGAACAGGGC	CCATGGAAATGGAATGTCCT	55	FP	710	1027	AAGACAGAGTCTG
Ya5ACA1504	AL590611	TTCGAGCCCATGGTAAGTTC	TGCAGCAGAATTTTAGACTTTCA	60	IF	179	499	AAAAAAAATTGTA
Ya5ACA1505	AL590617	AACTTGCAGCAAACACCGTT	TTGCAAGAGCTTGTTTTGTTG	55	FP	~130	453	NONE
Ya5ACA1506	AL034451	CTCCTGGAAGGATGAGTGGA	CCTGTGTGCATTTCTGTGTG	60	FP	~130	457	NONE
Ya5ACA1507	AL022477	TAAGGTCATCTCTTCCTTGC	TCTTCTCCTTAGGGTGTGAG	55	FP	75	374	AACTTCCTGAA
Ya5ACA1508	NG_002392	TGCAGACAAACATGGAATGAA	TTAGGGAAGAAGGGCTCCAT	55	LF	130	448	AGAAAGTTCATGGAG
Ya5ACA1509	AL357272	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AAAAAAACTTCGCATT
Ya5ACA1510	AL596028	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AAAAGAGTGTTGTC
Ya5ACA1513	AL513549	TGCCATTGTCATCAGCAAGT	TCTGTTTGTGGTTATGCCGA	60	FP	160	495	NONE
Ya5ACA1514	AL132670	GAATCACTACGGCTGAAGGC	AAACACCCAAGATTGACCCA	55	FP	155	469	AAAAAATGGGTACTA
Ya5ACA1515	AL356794	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AAAACAAGATAGCACC
Ya5ACA1516	AL359694	GGCAATTAAGGCACTGTGGT	ACCATGTTCCCTGATGTTCA	55	LF	165	467	GAAAAACTTGTG
Ya5ACA1519	AL139093	TCTCCCTATGATTTTATCTGCCA	TAGTGTGCCAAGGAAGCTGA	60	FP	60	388	AATAATTTC
Ya5ACA1520	AL450483	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AAAAACCACTGA
Ya5ACA1521	AL096770	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AAAAAGAACAAAGCTGG
Ya5ACA1524	AL512453	CTGTACCCATGGCAACCTCT	CTCTCCTGGAAGGAATGCTG	60	FP	146	465	AGAAAGCAAATGTGTGG
Ya5ACA1526	AL157823	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AAAAACAAACAAACA
Ya5ACA1527	AL161906	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	TACT
Ya5ACA1528	AL391595	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AAACTTTA
Ya5ACA1529	AL136094	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AAAAACAGTTGTG
Ya5ACA1530	AL033520	GCCAGCTGCATAAGGAGAAC	ACCAGCAACTAGGGACATGC	55	FP	108	429	AATACTTTCTCCTGGTG
Ya5ACA1531	AL513008	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AAAGACTTAAACTGG

(table cont.)

Ya5ACA1532	AL355997	CCCCTTGTGGCACATATAGAA	GCTTCATGATGTCCTGAGCA	60	LF	85	411	AAACAAGAGAGATA
Ya5ACA1533	AL133541	CCGGGGTCAAAGTACAACAG	CCAGACGTACAAATGCAAAGG	60	FP	174	483	AAAAATGCTCTTGA
Ya5ACA1534	AL035694	CAGTCAGAGAGTGCAATTCAGG	CGCTTTCCTTTGATCTCCAG	60	FP	124	445	AAAGGAAGTAGGGA
Ya5ACA1538	AL138722	CATGACCCTTGGCAAGAAAT	AAAGCCTTCCAGGACCTAGC	60	FP	177	485	AAACCAGGAATTC
Ya5ACA1539	AL450430	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AAAGAAGTGACAGGTC
Ya5ACA1540	AC021133	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AATGTTGAATATT
Ya5ACA1541	AL512363	TGTGCTGATAAAGATGACAGACAG	GTTTCAACCCTTCCTTTCCA	60	FP	655	965	AAAAACACAAAAATTAG
Ya5ACA1542	AL033397	CCCCAGGGATCTTCTTGAAT	TCTTCTCCCTTGACACACCC	60	FP	221	495	AAATTTAACA
Ya5ACA1545	AL137008	ATGCTGTGGCTGAGGAATTT	AAATTTTCCCGCTGATCCTT	60	FP	139	458	GATTTTTTCAA
Ya5ACA1547	AL590005	TCAGCATTACCCATTCCACA	TCTCCTGCCAAACAGACAGA	60	FP	139	447	AAAAATAGGAGGAGGT
Ya5ACA1549	AL356454	CTCTTTCCCAATGTCTCTCCTT	TGTGCCAGGAACTGTGTTAAG	60	HF	165	479	GAAAAGAAAA
Ya5ACA1551	AL590558	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AAGTT
Ya5ACA1552	AL354913	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AAAAAATCAATGAATTG
Ya5ACA1553	AL121934	TATGTTGGGAGGATGAAGAG	TCTGGGTCCACTCTAAGTCT	55	FP	134	474	AAGAAAGCGCAGGACAG
Ya5ACA1554	AL391807	CACATGTAACTAACCTGCACA	AGTTCATCCACATTTCCCTA	55	FP	135	490	AAATAAAAGGA
Ya5ACA1555	AL450164	CGGTTGGTTTCAATGTCCTT	TTTGTTGATCCAGTTTTATATGGC	60	HF	103	446	AAATCAAATTGAA
Ya5ACA1556	AL590678	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	GCCGGGC
Ya5ACA1557	Z98745	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	NONE
Ya5ACA1558	AL121972	NOT AMPLIFIABLE	NOT AMPLIFIABLE	-	NA	-	-	GAAAAATAT
Ya5ACA1559	AL049845	TTTCACCTTTACATATTGCCTACG	GTAGTGTGGATTACATTGACAAAA	55	FP	180	491	GAAATCTTTTTTTAC
Ya5ACA1560	AL096770	GCTTTTGGGAGAAGAACCAA	CCCACCTTTTCCTATCCCAT	60	FP	179	490	AAGAATGACAGCATGGG
Ya5ACA1561	AL121972	TGGATGAACTGTTGAAAAATATCAC	TGAAAAGAGAGTGGGGCAGT	60	HF	336	673	GAAAAATATCACTTTT
Ya5ACA1562	AL035466	CTACAGAACGCTCCACCCAT	CACTGTGATCCAAGAGTGTGG	55	FP	162	471	AAAAAAAAAAAAAACC
Ya5ACA1563	AL357075	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AAAAATGCATTG
Ya5ACA1566	AL157372	GCCATTATGCCAAGCAGATT	GAGGAAAGCACAACTCAGCC	60	FP	155	469	AAGACTTTCAGGCCAG
Ya5ACA1567	AL596028	TGGATTCAGAAACCTATGCAGTT	TAGTTTCAAGGGGTCCTCCA	60	FP			AAAAAATTTGAATC
Ya5ACA1568	AL355304	TTTCTTTACCTCATGAGTCATTT	ACCAATGACTTTCTTCACAGA	60	FP	87	395	AAAGTAGTTTTTTCC
Ya5ACA1569	AL356415	NOT AMPLIFIABLE	NOT AMPLIFIABLE	-	NA	-	-	AAAATGTACA
Ya5ACA1570	AL590428	AGAAAACTGCACATGTACCC	ACTGTGAAGCAGAAACATTG	55	LF	95	400	AAAAACTTA
Ya5ACA1571	AL731683	CCTCCTGCAAGAACTAAGCG	TCCAGTCAGTAGTGAAGGCATC	60	LF	110	425	AAGATGCCTTCAC
Ya5ACA1572	AL513188	CGTGGGGAAACTAAAGGAGA	TAACTTGCATTTCCCATTGC	60	IF	105	425	AAGAATGTAACC
Ya5ACA1573	AL391416	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AAAAACTCT
Ya5ACA1574	AL513210	AGGAGAATCACTTGAACCTG	GGATCAAGAAATGAAAATCG	55	LF	170	482	GTCTC
Ya5ACA1575	AL035694	CAGTCAGAGAGTGCAATTCAGG	CGCTTTCCTTTGATCTCCAG	60	FP	125	444	GAAAGGAAGTAGGGA

(table cont.)

Ya5ACA1577	AL139232	GGACCAAACAGTTGGAGCAT	AAACCTTTTAAACTTTCAGGAAAT	60	FP	104	418	AAGATTTCC
Ya5ACA1578	Z97205	TCTGGTGTTGTACTTTGTGCCT	AGGGAGGGGCATTAATTAGC	60	FP	~140	500	NONE
Ya5ACA1579	AL450328	GAACTGTTTTCTGGGCGCTA	TGGGATGTCAGTGTCTGTTTG	55	IF	186	493	AAAAAGATAGATGG
Ya5ACA1581	AL590785	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AGAAACTTTG
Ya5ACA1583	AL031446	TTGAAAAGATAAGCTGCACA	TTTGCATTTCCCTAATGACT	55	HF	229	556	AAAGAAGATATACAG
Ya5ACA1584	AL354857	GCGTCTAATCACACAGGCAA	TCATTGGGAAGCAACTGACA	60	FP	156	467	AAAAAATACTTTTCTGG
Ya5ACA1586	AL589947	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AAAATTCAGCTGTG
Ya5ACA1587	AL391336	GGGCAGAAGGACAATATGGA	GGGACTGCCTGCTTCTAATG	60	FP	162	466	AAAAAAGGACTT
Ya5ACA1588	AL365219	TTGCACAACAGCCTCCATAA	TCGTGTGGCTAGGTCACTTG	60	FP	69	382	AAAAAAGATGACAAGTG
Ya5ACA1589	AL590727	TGTAGTTTCATGGAAAGGGCT	ATTCTTTGGTGTGAGGTGGG	60	FP	179	487	AAGAAATAAGC
Ya5ACA1590	AC015920	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	NONE

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Ya5NBC8	AC006478	ATTAAGCACCAGGAAATTGCCATAC	CTAGTAAGGCTAGTCCCATAATTTGA	55	FP	196	513	AAGAACCTCATGATC
Ya5NBC17	AC007076	TATGCTCTGAGAGGTTTTCTAGATCTCTG	GAATAGGAGCATCATTCAAGTTCAG	65	FP	232	553	AAAAACAAATCA
Ya5NBC22	AC004519	TCTGTGTTCTTTGAATGTGTATTACTCTTA	GAATGTAAAGCTGTAACTTTCCT	55	IF	156	471	AAAAATTAAGGTC
Ya5NBC28	AC005862	GGGTACATGTGCAGGTTTCTTATAC	GCTAACTGATGAGAACACACAGATA	55	LF	191	474	CCCAG
Ya5NBC35	AC004534	GAGAAGTACTCAGAGAGGACATCATTT	GTAGTCATGGAGGTAAGAAAAGAA	60	IF	179	515	AAAAAACAGTCAGCAC
Ya5NBC36	AC004006	ATGAAATAACTCCTAGATTCAGGCTTC	AGTTTCTTGTGTTAGTTTCCTTAAATACCT	60	FP	145	545	CCGTCTCT
Ya5NBC38	AC006033	GTACCCTCTAATTTACAGTCATCTCATACC	GAACTTCTCTGGCTTGAAAAATCAG	60	LF	170	487	CCATTCCCTGATTTTTC
Ya5NBC67	AC006005	CACACACCCCGTATTTTCT	TGCATTCTCTTGGAGTTTG	58	FP	131	424	NONE
Ya5NBC78	AC006155	AACTCCAACAGCCACATCCT	TGGTGGGTCAGTATTGAGTGA	60	FP	66	382	NONE
Ya5NBC96	AC004547	TAGATGAGATAGAGCCATCAAACACTC	GTATTGTAACCCATAGAGCAACCAT	60	IF	169	509	NONE
Ya5NBC97	AC004453	GCTCTTTTCTTGTTTTCTGGAAGTG	TGTGAGTGTAAGAACACGTGTA	55	FP	147	442	TATTGTTGTTT
Ya5NBC106	AC005532	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	CTTCCCTTT
Ya5NBC107	AC004884	GTAATGAATAGCCGTGCAACTGTC	CACCCAGCCATTTCCTAGTTAT	60	FP	236	556	GAAAAGGATGCAG
Ya5NBC116	AC006344	GATCCTGAAACTATTTAAAATCAAGAAGAC	TCTAACCATATGTAGAGTTAATC	60	FP	237	575	AAGGAAATCAACTTT
Ya5NBC117	AJ010770	GGGAGGAGAAAGGAGAAACATCTAGT	CTCTCCAGCTATAACCCCAACTACT	60	FP	188	515	GGGGTTGGAATTTT
Ya5NBC119	AC006002	TGTTAATAAACAAGAACACTACTCCAAGG	CTTTTGTTATATATACTGAGGAGAAAATGG	60	FP	167	482	AAAAAGAGACATGAT
Ya5NBC128	AC004808	GGGTGGGACAAAGAAATACTCA	GCTTATGGCTTGCAGTTTCACT	55	FP	293	648	AAATAATGATGCTGTG
Ya5NBC133	AC000355	TGTTATCATTACACAAATACAGCACTTTA	TCTTTGGCTATAAGGATATGAAAAC	60	FP	374	692	GACATGGTGTTATTTTTT
Ya5NBC143	AC006374	GCAATGCACATAAGATATGCTC	CTTTTCCCTACCATGGTGTCTTT	60	FP	251	572	CATATTTAATGTT
Ya5NBC152	AC004953	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	NONE
Ya5NBC158	AC005019	TATCTCCCCCTACCAAATTTCTTTC	GGATGGATTAGAAAGGATGGATTAG	60	FP	172	500	GAATATAGATAATTTT

(table cont.)

Ya5NBC167	AC003980	AGCCCACAGCTAACGTTATACTAGA	GTGGGGTCTTTAAGGTTTCAATAG	60	FP	239	515	NONE
Ya5NBC169	AC002456	TATATAATCCCACAGTAAGCCCTCA	ATAGTTGTATACCAAGCCAACGACA	60	FP	184	493	AAAAATCCTTAGA
Ya5NBC177	AC000111	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	TGTTTCATTTCT
Ya5NBC179	AC006373	GCAGAAGCTTGCAATAACCTCT	GCTGAACACCTAAACACTGCTAGAC	60	FP	490	797	AAAAAAATAGTTA
Ya5NBC182	AC006365	GAAGGACTATGTAGTTGCAGAAGC	AACCCAGTGGAAACAGAAGATG	60	IF	287	563	NONE
Ya5NBC183	AC006365	GGACAGGTAGAGACGATTTCCTAGA	CAAGGGACTCATGTACTCTGTGAAC	60	FP	410	722	AAAATAAACAACTGG
Ya5NBC188	AC004970	GACAAGGACACAGATGTTAGGAATC	ATCTCTTGCAGTTGAATGTCTAAGC	55	FP	156	476	AAAAAACAAGCTAAG
Ya5NBC193	AC005065	GTTCTTTTTCTCTAAATGCCTCCTC	CCACATTTTTCTGGAACCACTTTAC	60	FP	206	525	ACTTACTTAAATTTCT
Ya5NBC194	AC004866	TATTCTTATGCCGTTATGTCCTCAG	CCATGGAATACTACTCAGCTATGAA	55	LF	169	486	AGAATAATGGGCTCCA
Ya5NBC200	AC005161	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AAAGAGTACAGACTC
Ya5NBC201	AC004745	CGCCACTTTCCCCAGTTA	CACCTCCCTAAAAAGCAGGA	50	IF	188	499	TAAGGCACT
Ya5NBC203	AC004593	CAGCCTGTAGAAGCTGGAAAAG	ATACAACAGTTCTGGAGGTCTGAAG	55	LF	128	445	GCCAACACCTTGATTT
Ya5NBC204	AC002385	AAGCAAATCAGTCCTACCATGA	TATTTTGGAGAGTTGTAGGCAGGA	55	LF	186	5199	TAGATTCTAATCTT
Ya5NBC210	AC004848	GAGGGGGTAGGGATAGCATT	GTGTTAATATTGTCCCCACATGTAA	62	IF	424	750	GCAGCTTATAATTCTTT
Ya5NBC212	AC002074	CATTTGGCGCAAGTGGTATT	ATCCCAAAGAAACCCACGA	60	HF	190	502	NONE
Ya5NBC214	AC004948	TGTTGTTGCAAAGGACAGGA	ACGTCCACATTCCCATGTTT	55	LF	170	500	ATCTATTCATCTGTT
Ya5NBC216	AC007245	GATGTGACCCTGGCTTGTAAA	CAGAGTCCCTGTGCAAAATG	55	IF	141	456	AGAACATACAGAC
Ya5NBC323	AC007076	TTGAAAGAGGAAGCCCAAGA	TCTCTGCTCCCCAACTCTTC	60	FP	268	556	TTTGTTTTT
Ya5NBC354	AC008039	GTAGCTTGGCCTGTGCTCTT	CCTCTGGGCTGAGAAACTCTT	65	IF	148	466	TCTTTTTCTTT
Ya5NBC361	AC007270	AATATTTTCTCCCATTCTTTTGG	TGTTAAAAGCGCAAGTCACAA	60	IF	131	423	GTCTTCACTTTCTT
Ya5 412	AC006033	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	NONE
Ya5 422	AC004946	CCGAAAGAAAGGACCAAAGTC	CGCAATGAGATGTCCTTCAA	58	FP	124	440	AAGACTGAAAAA
Ya5 429	AC002383	TGGTTTCCATTAGGCACAGG	GCATGTTGTGCACATGTAACC	60	FP	131	456	CCATACTTCT
Ya5 441	AC004945	GTCCTTTGCAACATGAGTGG	GGTGATGATGGGGTAGCACT	60	FP	200	520	GTCTATTGTA
Ya5 451	AC004547	GCCATCAAACACTCTTGACCT	GGAGCTATGCCACAGAAAGG	61	HF	135	475	CCATCTTTCTCTGATCTT
Ya5 457	AC004028	CCCACTGATCCATCAGCTCT	CGTTCTGTATTTGCAACTTGTG	60	FP	88	402	AAAACCAAGAAATC
Ya5 460	AC003075	GCAAACTTTAGTGATACCACATTCC	CGGGCTGATTTCATATCCTG	60	FP	93	411	TCTGACAATATTTTT
Ya5 461	AC003080	TCAATTCCAAGTTCCCCATC	GCCTAACACTTCTGACCTTTCA	60	FP	99	414	NONE
Ya5 462	AC003045	AATGGAACTGAAAGGCCTGA	GGATCCTTGGGTTCAGAACAT	60	FP	114	431	NONE
Ya5 465	AC002542	CCTCCAAAGACAACTACTTAATGG	GGTACACAAACATAAGGACAGTTTC	55	FP	230	496	GTCATTCC
Ya5 469	AC002080	TGGTCACCAATCCATGATTTC	GCCACAGGAAGGATGGTGTT	60	FP	97	402	AAGGAAAAGA
Ya5 495	AC011290	GCCTTAGTGTGGCCCAAGT	CAGCCCCAAACCTTGACTTA	55	IF	138	452	AAAGGATACAACT
Ya5 497	AC005047	CATCTCCTATGGGGGAAAAA	TTCAGTAAGGAAGGCGGGTA	55	FP	128	451	AGAAATGTGTG
Ya5 505	AC007245	GATGTGACCCTGGCTTGTAAA	CAGAGTCCCTGTGCAAAATG	60	IF	128	456	AGAACATACAGAC

(table cont.)

Ya5 506	AC007245	CCATGGAAAGCCACAGTTTT	TGTGTGCATTATACAGAGACATGC	58	FP	140	457	AAGAATCAAAGATCAT
Ya5 524	AC009517	GGCAATCTGACCTTGGGTAA	GGCTATTCAAGTGGCCAAGA	60	IF	310	605	CAGAAGTTAGAT
Ya5 526[2]	AC058791	GCTCCATGAAAAACCCTCCT	TGATGGGAAATATGTGAGTTCG	60	FP	304	641	AAAGATATTTCTT
Ya5 539	AC005161	GTTGTAGGTTGGGGATGGAC	CCTTCAGATGTTCCCCATTG	60	LF	89	417	AAAGAGTACAGACTC
Ya5ACA1591	AC004453	CACAACTTTGCAGCCTTGAA	GGGAAAACCCACACATGACT	60	FP	173	468	AAACAACAATA
Ya5ACA1592	AC009331	ATTGGCTTGTGGATATGCCT	AAGAAATGCTCCACCCCTTT	60	IF	516	850	AAAAATTAGCCGGATG
Ya5ACA1593	AC005250	AAAGCTTGTTTCATCCTTCA	TTTTATGTTGCAAGAAGTAAGG	60	FP	159	473	AAAAACAATGTC
Ya5ACA1594	AC005072	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AAAGTCCATTTGTG
Ya5ACA1595	AC004965	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AAGAGAGTGAGGGGGC
Ya5ACA1596	AL035067	TATTGCCCTAATGACCTCTC	TGAATAGAAAAGATGACTACAGGA	60	FP	249	578	AAAACTGATCATGT
Ya5ACA1598	AC004884	CCCAGCTGGTTTTTCTAAATG	AATAGGCGAGAGGGAATGGT	60	IF	142	460	ATTGTTAAAATTTAA
Ya5ACA1599	AC007393	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AAAAATTTTA
Ya5ACA1600	AC079355	GGTGGCTTGTCGTAAATCGT	CCCTATGGCCTGCTTATCTG	55	FP	130	442	AAGAACACAG
Ya5ACA1601	AC104073	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AAAATAAGCACTTGTGG
Ya5ACA1602	AC004691	NOT AMPLIFIABLE	NOT AMPLIFIABLE	-	R	-	-	AAAAATTAT
Ya5ACA1604	AC005046	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AAAGATTTACCCTT
Ya5ACA1605	AC005046	AGCCATTGGAATAGTGGCAG	ATGTTACCACCAACTCCCCA	55	FP	158	478	AAGTTTGGGGAGTTGG
Ya5ACA1607	AC006997	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AGAAAAAAATTA
Ya5ACA1611	AC073626	TTTTGGTAAAGATGCCACAGAA	TCCTAAACATAATACGTACAGGTGA	60	IF	184	496	AAAACAAAAATATTGTC
Ya5ACA1612	AC073901	CTGGCTGCCAATTATGTGTG	AAGCTCAGTGTGACCGTTTTT	55	FP	131	421	AAGATATATTGATTGC
Ya5ACA1613	AC003080	GCCCAGTTGTCCACTCAAAA	TCAATTCCAAGTTCCCCATC	60	FP	138	453	AAAAAATTAACACAC
Ya5ACA1614	AC092148	TAGAGACAGAGCTGTGGGGC	TCTCACCCGAGGAGATGTCTA	55	FP	200	493	AAGAAATGCTATTTGT
Ya5ACA1616	AC073042	TGATTCCACCAGAATAGTGACA	GGACTTCCCCTTACCAAAGC	60	LF	111	466	GAAAGTGCAGTCTGG
Ya5ACA1617	AC002542	NOT AMPLIFIABLE	NOT AMPLIFIABLE	-	NA	-	-	AAGATAGCTTCGAG
Ya5ACA1620	AC002080	GCTTGAGCAGTGACACCAGT	CTGGGATTACGATCCTGTGG	60	FP	171	490	GTTAAGG
Ya5ACA1622	AC073145	CATGCTTGCCAGAACAGAAT	GATGCTGGTTTTTGAATGGC	60	IF	158	476	AGAAATTATAAAACAG
Ya5ACA1623	AC006964	ATTGTGCCACTCTACTCCAG	GTCTCGCTAAAAGCAACATT	55	FP	262	600	AAAGAAAACAAAC
Ya5ACA1624	AC073054	TTTCTGTTGTCTCATGTTTTTACCA	AGCATGGCACTTTGGCTATT	60	FP	168	482	AAGAAAATCTTTC
Ya5ACA1625	AC024952	TTCATTAGCAAATCCCGAGG	GATGGTCGCTTGAGTTAGGG	60	FP	85	406	ATATATTCTG
Ya5ACA1627	AC008039	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	GAATTTGGG
Ya5ACA1628	AC093183	NOT AMPLIFIABLE	NOT AMPLIFIABLE	-	NA	-	-	AAGAGCTGGTGTTCA
Ya5ACA1630	AC011005	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AAAAAATAAAATTC
Ya5ACA1631	AC010655	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AAGAAATTGCC
Ya5ACA1633	AC004006	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AAAGCCATGATA

(table cont.)

Ya5ACA1636	AC024082	GTCAAGGCTGTATCCAGAAG	CATTTTTCCCCTGAATACCT	55	FP	72	347	AAACAAATAT
Ya5ACA1637	AC009245	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AAAACCCACTGAG
Ya5ACA1638	AC074089	TGTCCTAGCCCCTTTGACAC	TGCAAGGCATTCTGGTATTG	60	FP	143	479	NONE
Ya5ACA1639	AC004859	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AAAATTAAAAACTT
Ya5ACA1640	AC083849	NOT AMPLIFIABLE	NOT AMPLIFIABLE	-	NA	-	-	ATCAG
Ya5ACA1641	AC004543	GGCTTAATTGCCTTGCTCAG	CCACAAACATAATAGGGATTTTC	55	FP	154	497	GAAAATCCC
Ya5ACA1642	U66059	CCCCCAAGAAGTTGTCATGT	TTGAGCAATCTCTGGTCAGC	60	FP	162	482	CGCTGACCAG
Ya5ACA1645	AC002383	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	GAAATATGGGTAGTGAG
Ya5ACA1646	AC006315	CATGAATTTCCAGTTTCGGTG	CTACTGGCTTCTCTGCGTCC	60	FP	198	491	AGAACTTGG
Ya5ACA1647	AC007130	AGGTGAGAGGGTGGTTAGGG	TGAGGCTCCACTTTTTGAGG	60	FP	130	448	ACTAGACATTT
Ya5ACA1648	AC005084	GCCTCACAGTTTGGTTCTATGG	GGACCTGCATTTGCTTTCTT	60	IF	176	499	AGAAAATACAGAAATTG
Ya5ACA1649	AC006006	TCATTTGTTATCTTCTGTTGGTTGA	AGGCCGGGTTCTAAGACCT	60	FP	162	478	AGAAATTAAAACATA
Ya5ACA1650	AC009517	ATTCCCTTTCCTCCAGTGGT	GGCAATCTGACCTTGGGTAA	60	IF	183	493	AAAATCTAACTTCTG
Ya5ACA1652	AC012557	CTTGACACCTGCTGTGAGGA	CGTGAAGTTAATTGCTGCCTC	60	FP	145	453	AAGAAAAGGAGG
Ya5ACA1653	AC008080	CCTGCTCACTGCTTTTGCTT	CACCTAGGAAGGGTTAGGGC	60	LF	150	481	AGAAAGCCAGGCTCA
Ya5ACA1654	AC005862	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	NONE
Ya5ACA1655	AC018641	TACCCCAATTCTCATGATGC	TTCAAATTGCATTTCCATGA	55	FP	131	468	AAAAAAAGTAGTACA
Ya5ACA1656	AC006350	GGGCTCTGGATCTAAAAGCA	AACCAGATTTGTGCTTTGCC	60	FP	189	460	AATGTAAC
Ya5ACA1659	AC073236	TTGCATCTTCTGAGGCAATG	AGGGGGTCAAGAAAGGAAGA	60	FP	655	930	CATTGTC
Ya5ACA1660	AC005076	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AGGCC
Ya5ACA1662	AC079987	TGGACACAATATGGACTAAAAGGA	ACACTTTGGCAGAATTGGCT	60	FP	140	454	AAGAAATACAGTTG
Ya5ACA1664	AC005039	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AAAAGATCCCCAATT
Ya5ACA1665	AC007035	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AAAACCACAATGAG
Ya5ACA1666	AC091439	TGGAAACAAAGGACAGGCTT	GGGCAAAGCTACACACTTCG	55	FP	160	482	AGAAAAGGAATATTTAG
Ya5ACA1667	AC073878	TGTCAGTGGCCTGTGAGAAC	TCCTCTGTCATGTCTTCTTTTCC	60	HF	154	432	AAAACCTCTGTAGA
Ya5ACA1668	AC004833	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AAAGGG
Ya5ACA1670	AC012590	TCCTGACTTCTATGTCATTGTTGAA	TGGCAAAAATGTTTAAAGTAAAAG	60	FP	147	459	AATTTCA
Ya5ACA1671	AC010971	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AAGAAAAACAAAATT
Ya5ACA1672	AC073150	GCACATGTAATGGGGCTTTT	GGGCACTGTACAAAATGCAA	55	IF	162	437	AAAAAATTACATAT
Ya5ACA1673	AF027390	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AATAAATAAATAA
Ya5ACA1674	AC082648	TCAATGGATCCAAAAATTCCA	CCAGTAGCACAACAGCCTCA	55	FP	132	448	AAAGATTCACTCTTTTT
Ya5ACA1676	AC073347	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AAAAATATA
Ya5ACA1677	AC073136	AAAAATCAATGAAATAAGAAGCTGG	TCTGCAGCAATATCCCAGAA	60	FP	156	482	AGAAACTGACAAAAATAG
Ya5ACA1678	AC104073	CAAGACTATCCCCCAGGCTT	CCACCTCTGATCCCATTGAT	60	FP	100	446	NONE

(table cont.)

Ya5ACA1679	AC073422	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AAAAAAAAAAAAAGG
Ya5ACA1680	AC073472	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AAAAGAAAAGACCA
Ya5ACA1681	AC005531	AATGCGCAGACTAAGAGTTT	CCAAAGTTCTAGGATTGCAG	55	FP	68	383	AAAAGGGGCCGGG
Ya5ACA1682	AC005081	TTCATGTTGATTGGGCAAGA	CCCAGGAGGGTTTGTGTAGA	55	FP	630	847	AAAAATAAGAAAATTAG
Ya5ACA1683	AC114501	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AGAAAGTGATGGAATGG
Ya5ACA1684	AC006337	AGGACAGGAAACAAATCCCC	CTCCAGGGTGTTCCCATAGA	55	LF	151	470	AAAAAGAAACCCA
Ya5ACA1685	AC114489	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	GAAGA
Ya5ACA1686	AC018720	TTTTGGGGCATTCAGAAGTC	GGGCAGAAAATAAGTCCAAGG	55	FP	119	452	ACCTTGGACTT
Ya5ACA1687	AC093685	CCATTTTGGAACCTGCTTTG	TAACCAGCACTGGGGAATTT	55	FP	158	474	GGCGACAC
Ya5ACA1689	AC092676	TGAGGGTATAAACAGAGTGCCC	TTTTTCCTATCCAAGCGTGA	55	FP	168	476	AAAAAGTGGTGGG
Ya5ACA1691	AC005077	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	NONE
Ya5ACA1692	AC114737	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AGTTTAATTC
Ya5ACA1693	AC114737	CTCAAAGCTCAGAGGAGGGA	ATCCTACTCTGCTCCAGCCA	60	IF	80	396	AAGAAATAGCCA
Ya5ACA1696	AC004987	TGCAGGTCCATACCTGAGTG	CATAGGTTGGGAGAGGTGGA	55	HF	162	472	AAGAAAATTAAA
Ya5ACA1697	AC006204	TATTTGGGATGCAGCTAACG	TTCTTCTGCTAACTTCGGGC	60	FP	155	465	AAGAAGTTAGA
Ya5ACA1699	AC104692	NOT AMPLIFIABLE	NOT AMPLIFIABLE	-	NA	-	-	AAAAATTGAGACGTGTT
Ya5ACA1700	AC007245	NOT AMPLIFIABLE	NOT AMPLIFIABLE	-	NA	-	-	AAAGATCAT
Ya5ACA1702	AC073181	TCCCCCATCTCTTTTTCCTT	TGGATAAAGCTGCAACACCA	55	HF	112	454	AAGATAAAGACTTTTGG
Ya5ACA1704	AC004848	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AAAGACTTGGAACC
Ya5ACA1705	AC006365	NOT AMPLIFIABLE	NOT AMPLIFIABLE	-	NA	-	-	AGATG
Ya5ACA1706	AC004889	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AAAAAACAGTCAGCAC
Ya5ACA1707	AC073111	CCCAGTCAAGGGAGAACGTA	CAGCAAAGACCATCAAAGCA	60	FP	674	988	TCCCCCATGTC
Ya5ACA1708	AC005079	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AAAAACCACAATGAAA
Ya5ACA1710	AC024082	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	NONE
Ya5ACA1711	AC083869	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AAAAGATATAAAATATT
Ya5ACA1714	AC012351	CATGTACCAAGCAGTTTGAA	AAAGTGCTCCCGAAGTACA	55	FP	176	490	AAAAGATGCCTGAAGGGG
Ya5ACA1715	AC091439	TGGAAACAAAGGACAGGCTT	GGGCAAAGCTACACACTTCG	55	FP	160	481	AAGAAAAGGAATATTTAG
Ya5ACA1720	AC006153	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AGAAAACCCC
Ya5ACA1721	AC004008	GTTTCAACATGTAACCAATGAG	TCAGAAGGGTAAGCTCAAAG	55	LF	141	470	GAGAAACTTTGG
Ya5ACA1723	AC023669	GCTCTTTCATCCTCACTGGC	AATCTGACCCAGGTGTTTGC	55	FP	471	793	AAAAATAGCAAACACCG
Ya5ACA1724	AC073900	ATCCCATTGATTTTGGCAAG	GATCCTTCACTTCAGCCAGC	55	FP	108	415	AAAAAGACATGG
Ya5ACA1725	AC002540	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AAAAGAATGGAAATCAG
Ya5ACA1726	AC002429	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AAAAGAGAC
Ya5ACA1727	AC004745	TTCTTGTTCATCACAATGGCA	TGAGTACCTTCTTCGCCACT	60	IF	218	460	AAAAACCTCAGTCCTT

(table cont.)

Ya5ACA1728	AC073324	CACGTTAACAAGCCACGAGA	AGGAGAGAATCCAGGGGAAA	55	FP	133	440	AAAAACCCTCCA
Ya5ACA1729	AC010677	ACAAAGCAGCAACAAACCCT	TACCCAATCCCACTGATGGT	55	FP	169	489	AAGACTGGTAACTTG
				-				
CHROMOSOME 8				-				
Ya5NBC356	AF130343	CAGGGTCCTGTGAATCCAAT	GGAGACAGAGAAAAGGGGAGA	62	FP	84	389	CACTTTGTTCTTTT
Ya5 482	U67217	AATCACAAATGCTGGTAAGTGC	TGACAAACTTAACTGATCTGAATCA	58	FP	182	458	AAAAAATAATGT
Ya5 516	AC008066	TGGAAGGCTGTAAACCTTGTG	GGGCAGGCAACTAACAACAC	60	FP	101	405	AAAAGTGATTTGGAG
Ya5ACA1731	AC015807	TACTTGGTAGGCATGGACCC	CAAGCTGCACTGCTTTCAGA	55	FP	163	474	AAGACTTCCGGGTTC
Ya5ACA1732	AC090816	GTAAGTGGCAAGAGGGTCCA	TTGCTAAAGTGCAGAGGAACA	55	FP	143	458	AAAATTCCTAAATCG
Ya5ACA1733	AC090987	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AAACAAAAAACACTTC
Ya5ACA1734	AC106727	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AATAATAACTACA
Ya5ACA1735	AC025615	NOT AMPLIFIABLE	NOT AMPLIFIABLE	-	NA	-	-	NONE
Ya5ACA1736	AC104716	CCTGCTCTGCACACTTCTTG	GCTAGTCAGGGAAACAACAGG	60	LF	141	484	GCCTTCTC
Ya5ACA1737	AC022274	CAACATGAGTGCTTCCTCCA	ATGACTGTGCTTTGGCATCA	55	FP	167	491	GAAATATAGTTTGA
Ya5ACA1738	AC011974	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AAAAATTGGCCAGTATC
Ya5ACA1739	AC062004	CCACAGCCAGTGTTTATGGA	GGCATTTGCAAGTTGGCTAT	60	FP	540	907	NONE
Ya5ACA1740	AC104018	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	CAACCTCACC
Ya5ACA1741	AC025599	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	GAAAATTGCTAAGAC
Ya5ACA1743	AC091050	TGTGATCACCTTCCCTCTCC	GGACTGCAGTTTGGCTTCTC	60	FP	178	485	AAACCCCAGAGGA
Ya5ACA1744	AC100800	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	GAAAAGAGAGGAAGATG
Ya5ACA1745	AF165145	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AAGAAGCTGA
Ya5ACA1746	AC112673	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	TGCTG
Ya5ACA1747	AC040970	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AAAGGTAGG
Ya5ACA1749	AK023771	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AAAACACTACTCAC
Ya5ACA1750	AC009107	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AAGAAATTCATATATGCA
Ya5ACA1751	AC022260	TGTTTTCCCAGAGTTTTGCC	AGGTCAGTGGGAGACACCTG	60	FP	675	997	AGAAACTC
Ya5ACA1752	AC021842	TCCTAGGATAAGTATTTGGTGCC	GCTCAGATTGGGATAGGAAAA	60	FP	172	492	GATTAATAAA
Ya5ACA1753	AC092709	TTGAAAGAGAAAGTGATCATATCCA	TGACCTCTATTTTCAGCGGG	60	FP	169	480	TTTCCTTTCTA
Ya5ACA1754	AC022833	TTTGGTTGAAAAGGAGGTGG	CAGTAGTTCTTGGATGGGGC	60	FP	148	459	AAAAAAAAAAGTAG
Ya5ACA1755	AC079054	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AAAAGAAACACAACTGAG
Ya5ACA1756	AC136590	CCATTGAATTTTCAAAACGG	TGAGCATCTAGTACCAGCTCTGAC	60	FP	132	454	AATAATTTAGTG
Ya5ACA1757	AC024681	AGCCCAGCACCTCTGAAGTA	CAGTTTAGACTGCCCCCAAA	55	FP	451	764	AAATAGCCGT
Ya5ACA1758	AC091189	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AAAAGCTACAAAGAT
Ya5ACA1759	AC009634	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AAATAAAAATTTA

(table cont.)

Ya5ACA1760	AB020864	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AAGAAGCTGA
Ya5ACA1761	AC090186	TAACATTTTCTGGGAGGAAC	TGTAATCCCAGCTACTCAGG	53	FP	149	498	NONE
Ya5ACA1762	AC020937	NOT AMPLIFIABLE	NOT AMPLIFIABLE	-	NA	-	-	AAGAACTAGAAATTC
Ya5ACA1763	AC021236	ACGTATCAACTGATTCCCGC	CACCTGACAATACCCTGGCT	60	FP	545	863	AAAAGAAAACATATG
Ya5ACA1764	AC022887	CGACAGAGCAAGATTGTGT	TGGCTACCAAATCATTAACA	55	FP	190	490	AAAAATATAT
Ya5ACA1765	AF198095	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AAGACTGCGTA
Ya5ACA1766	AC132834	CATCATGGTATCCCAAGCCT	TTCTTCTGGGCAGTCTGTCA	55	IF	154	471	AGGACAGTGTC
Ya5ACA1767	AF189005	AGACTTCTCTGATGGGGCCT	AGAACTGAAGGCCATTGTGG	55	FP	140	468	AGAAATT
Ya5ACA1768	AC091173	NOT AMPLIFIABLE	NOT AMPLIFIABLE	-	NA	-	-	AAAAAAACAGAGGG
Ya5ACA1769	AC103779	CCAGAGAAAGCATAAAAGGCA	CCAAACTTACATTTTTCTGCCC	55	FP	153	460	AACATGCTTTT
Ya5ACA1770	AC103688	CCCCAAGTAGCCTGTCAAAA	CAGGCAGCATCACTACCTGA	60	HF	222	473	AAAGGAAGAC
Ya5ACA1771	AC020588	TCCGCACACATAAGCACTTC	TTGGCAGGAAAGGTCTATGG	60	FP	182	494	AAAATAACTCAATAT
Ya5ACA1772	AC100798	TGTAACCATAGGTTGGGTTAAGA	TCCAAGTGTATGTTTTGCCT	55	FP	153	469	AAAAGAAAACGATTGC
Ya5ACA1773	AC019031	CCATTGCCCAGCTTAAGAAA	GAAGGAGAGGAATGCAACCA	60	FP	83	405	AAGAAATACAGCCTCG
Ya5ACA1774	AC090136	TTGGAAGAAAGCCTTGAGGA	AGCTGTTTCCACCCAACATC	55	FP	161	477	AAGAGGACTTGTTTC
Ya5ACA1775	AC022790	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AAAACTCATAACCTG
Ya5ACA1776	AC018437	GGATGATGAGAAGGGCTACG	TCAAGGTATTTCCCCTTCCC	60	FP	48	377	GGAAGG
Ya5ACA1777	AC104384	TTAAACAACATTCTGGGTTTACAA	GAAATTCTACAATATTGGTTGTGC	55	FP	138	434	AGAGAAAGCAC
Ya5ACA1778	AC104000	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AAGATGTCAATTTTG
Ya5ACA1779	AC025615	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AAAACTTGTTTGTGG
Ya5ACA1780	AC090821	GGGAATGTGTTATGCCCATC	GAGGGCAAGAGGATAGGGTC	60	FP	570	895	AAGAATTTTAGA
Ya5ACA1781	AC022039	AGAGTAAAACACCATAAGCATTTGT	TCCATTGCCTTCTCAACCTAA	55	FP	138	426	AAGAATTA
Ya5ACA1782	AC040914	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AAATTAGGACCTG
Ya5ACA1783	AC009686	TTTGTTTCTTCAGAATGGCCT	AAACACATTTTCGATGCGGT	55	FP	154	469	AAGTA
Ya5ACA1784	AC073192	ACCAATGGCAAGTCCAAGAC	ACAGTGATGGGACCTCCAAG	55	FP	168	482	AAAAGTCAGGGATGT
Ya5ACA1785	AC019215	TCCTCTCACCCAGAAAGCAG	ATTAACCCATCTCCTTGGGG	55	LF	159	479	AAGGTAATAATAG
Ya5ACA1786	AC112673	CCCTGTTTGGCAGATGAAAT	CATGGCCATCACAACAGAAG	55	FP	170	491	NONE
Ya5ACA1787	AC018540	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AAAAAATAATAATA
Ya5ACA1788	AP000501	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AAAGAAATAAATAA
Ya5ACA1789	AC007991	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AAGAAATAATATTTAA
Ya5ACA1790	AF202964	AAAAGGGAGTCAAGATTGAAGAA	TGTTTTTCCTGTACTTAAGTGGCT	60	FP	187	498	TTTAAAAA
Ya5ACA1791	AC027259	TTCCAAACACTTTGAGCCAG	CTTTGTTTGCAGACGGCTTA	55	FP	145	371	AAAAAAAAAGATTTA
Ya5ACA1792	AC093329	TCCAAGAAACAAAGGAAGAG	TTTCAGCATGTTGACCAGTA	55	FP	189	456	AAAAAGAAATCAGTCA
Ya5ACA1793	AC025522	TTTTTCCAAAAATGCTGGGT	GTTCATTGACTGGGTGGGTT	55	HF	165	492	TTGCCCCTTTC

(table cont.)

Ya5ACA1794	AC004612	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AAGAAAGTTGA
Ya5ACA1795	AC069353	CTCCCAAGGGACTCACTCAA	AATAAGGCCAGTGGTGTTGG	60	FP	145	462	AAGAAGAAAAAATA
Ya5ACA1796	AC007992	CAGAGCAGACGTTGACCTTG	TCCCACAAGTCACAGTTCGT	60	FP	164	472	AAAAATACTTTT
Ya5ACA1797	AC018801	GCTGGCTGTTAGGGATCAAA	GTGCAGCGATGGTAGGAAAT	60	FP	514	868	NONE
Ya5ACA1798	AC083836	NOT AMPLIFIABLE	NOT AMPLIFIABLE	-	NA	-	-	AAGAACCTGAGGGAA
Ya5ACA1799	AC025207	TTGAAAATGAACAAACAGGGC	CCTTTCTTGACAGCTCAGCC	55	FP	104	414	AAAAGGTGACTGCA
Ya5ACA1800	AP003534	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AAAAAAAATTGAAATTA
Ya5ACA1801	AC105193	TGTCAGTTTTTCATACTTGAAATGG	TTGGTACATTTGTGGGGGAT	60	FP	181	496	GAAAATAGC
Ya5ACA1802	AC010859	GGTTGCCACATCCTATGGAG	TGGGCTTTTAGTTCCACCAC	60	FP	110	424	AATGTGG
Ya5ACA1803	AC018781	CTCATGTTTTGATCTTCCTAGTC	ATTACAGGCATGAGCCACT	60	FP	86	400	AAAAATTAGAAATTG
Ya5ACA1804	AP003357	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AATTTCCTTAGTC
Ya5ACA1805	AP003438	AAAAGGCAATACATGGCTGG	TGATGGGATTAGCACCACAA	55	HF	88	412	AGAAAATATGGGAC
Ya5ACA1806	AP003477	TCAATGGTACAACCAAACAACA	CCCTACTGCCTTCCAACTTTT	55	HF	191	500	AAAGAGAATA
Ya5ACA1807	AC055820	NOT AMPLIFIABLE	NOT AMPLIFIABLE	-	NA	-	-	ATAAAACACACTTTA
Ya5ACA1808	AP003115	AGAGAGGGAGTTTTCTGCCC	TCAAAGTCCTCATGGTGGAA	55	FP	160	485	NONE
Ya5ACA1809	AF363578	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AAAAGTTATGTT
Ya5ACA1810	AP003356	CCCCGTCAGAATCACAAGTT	GGCGTATGCTTTAGGCTCTG	55	FP	600	957	NONE
Ya5ACA1811	AL160408	CACACACATAGACACAGAGCCC	CAGACCACAGACCAGTATGGC	55	FP	166	500	NONE
Ya5ACA1812	AC025508	NOT AMPLIFIABLE	NOT AMPLIFIABLE	-	NA	-	-	AAAACTAAATCAG
Ya5ACA1813	AC120042	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AAAAAACTGGACCCTG
Ya5ACA1814	AC019357	TGATTTTGACTTAGTATTGGGAAGC	TAGAAAACAGGCAGGGTCCA	55	FP	74	397	CTGGACCCTG
Ya5ACA1815	AC108008	CCAGAGAGAAAACCTTTTGGG	GCATGGCTATCCTAGCTTCTG	55	FP	113	424	AAGATGAAAGATG
Ya5ACA1816	AC068399	GCCCAAACTCTGGATTTTCA	TGGTTTGGATTCCACATTGTT	55	FP	84	412	ATAAATGTTGACTCTA
Ya5ACA1817	AC022360	GCTAGCTAACCTCAGAACTATCCC	ATTGCTGGTGGGTTTTCATC	55	FP	73	406	AGAACTACTTGGAAAA
Ya5ACA1818	AC064802	TTCAGAAGAGTGCACAAAGTCAA	CCATCAGCATGCAGACACTC	55	FP	138	450	AAAAAAGGAACCT
Ya5ACA1819	AF178030	NOT AMPLIFIABLE	NOT AMPLIFIABLE	-	NA	-	-	NONE
Ya5ACA1820	AC055822	NOT AMPLIFIABLE	NOT AMPLIFIABLE	-	NA	-	-	AAGATAATGGGCGA
Ya5ACA1821	AC087361	CATGTGCCATGTAACCAAGC	TCCATCTTTGCAGCTCAGTG	60	FP	62	378	AAAAAAGACACTGAG
Ya5ACA1822	AP002905	GGACAACATTTTGGTCCTTCA	ATTGTTTTCCCCTGCCTTCT	55	FP	140	467	AAAAGTATGA
Ya5ACA1824	AC107628	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	NONE
Ya5ACA1825	AC011884	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AAAAGACTAGGGTGGG
Ya5ACA1826	AF235104	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AAGATTCTTCCATGT
Ya5ACA1827	AC062004	CCACAGCCAGTGTTTATGGA	GGCATTTGCAAGTTGGCTAT	55	FP	576	896	AAAAATTCTATATTACA

(table cont.)

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Ya5NBC33	AC006288	GCAATTGCTATCCTTGAGTGTTTC	CTCCTAGTCTAGAGTTTTTCCCAT	60	FP	226	543	AGAGCCT
Ya5NBC175	AC000396	CCAGTGTCATACGGTGCTTAAATC	GGACTGGGCTCTTCAGGAC	55	FP	148	483	GAAATACAAGGTGCC
Ya5NBC184	AC000047	CTTGGATAGAGCTGGAGGTCATTA	ACCCAAGCAGTTTATACTGTACCC	60	LF	205	522	AAGAGTGATTAATGG
Ya5 418	AC006288	TGGTGCAATTGCTATCCTTG	GCATATCTGGGCAGGGACT	55	FP	64	381	AAATTTAGAGC
Ya5 463	AF029308	TGAAAAGCAGAGTAAGTGCTCA	CGAAACAAATCATGCCTGTG	55	FP	150	472	CATTGTGGTCAA
Ya5 479	U67222	GAGGCCATTCTCTAGGTTGC	GAGGCTTAAAACAAGGGAGGT	55	FP	172	492	AAGATTATAATTTGTG
Ya5 480	U67220	AAAAGAAGAGGATGTGGGAAAC	TTTCAACACTGCTTGGGTCT	60	FP	149	443	AAAAAAGCCTTGCTTAT
Ya5 546	AL133479	TGCCATGACATTTTCCAAATA	GAAAGGAGTGGTTAAAGAGGAAGA	55	FP	165	486	CCAGTTTAGTTTCTT
Ya5ACA1828	AL513333	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AAGAAGATATAATTA
Ya5ACA1829	AL451045	GCAGGTCTCCTTAAGACAGCA	TGACAAGAGTGGCAAGTTGG	60	FP	65	386	AAGACAGCATACAG
Ya5ACA1830	AL355592	TCCTTTTAGAAAAATCAGCTGTCC	TCAATGAAACATGAGGAAGCA	60	FP	98	435	AAAAATCAGCTGTCCTG
Ya5ACA1831	AL365201	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R			AACAATATGGTAAACCT
Ya5ACA1832	AL158073	CCCCTGTGGTTTTCTTTCCT	ACAGCCTGACTTGCCTTTTG	55	FP	145	458	AAAAGGAACAGAAGAG
Ya5ACA1833	AL355604	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AATAATAACATTTA
Ya5ACA1834	AL359091	NOT AMPLIFIABLE	NOT AMPLIFIABLE	-	NA	-	-	NONE
Ya5ACA1838	AL392163	TCTCATGGTATTACCTTCTCATCAA	TCACCAATCTCTCAGCCTCC	55	FP	137	444	AAAACTTACAAAGT
Ya5ACA1839	AL445252	CTCCTATCATGAAGGGCTGC	GGTCCTTTGTTTCAGTTCCG	60	FP	139	461	AAAAGAAATAGATTTAA
Ya5ACA1840	AL133476	TGACCTGTTGAAATGTCCCA	TGCTCAAGCTACTTGGGTGA	55	FP	161	477	AAAGTAGAG
Ya5ACA1841	AC011701	TGGTCAGTGTCTGGAGCAAG	CAGTTATGCCCCATGGTTTT	55	LF	166	456	AGAAATACAACTTGCA
Ya5ACA1842	AL163528	CAGGGAAAAAGAGCAACCAG	AATCCAACATCTTTGCCCCT	60	FP	56	375	AGAAACTGTATTTGA
Ya5ACA1843	AL357615	CAAAGATTCAGCTTTCAGCTGTT	TGAAAAATAAAAACGTGGGTGA	60	FP	111	419	AAAATTTC
Ya5ACA1844	AC006312	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	NONE
Ya5ACA1845	AL353772	NOT AMPLIFIABLE	NOT AMPLIFIABLE	-	NA	-	-	AAAAAGTACAAATAT
Ya5ACA1846	AL359636	TGGCCAGAAGGAAGGAAGTA	GGAAAGTTTGGGTCTGTGCT	60	FP	194	498	AAAGAAAAAGCTA
Ya5ACA1847	AL162396	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AAAAAGTTAGAAAG
Ya5ACA1849	AL392110	NOT AMPLIFIABLE	NOT AMPLIFIABLE	-	NA	-	-	AAGAAATGAGATTTGTTC
Ya5ACA1850	AL158822	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AAGATTACTG
Ya5ACA1851	AL445467	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AAGAGTAGCCTC
Ya5ACA1852	AL353607	TCAAAACTGGACCTTTGAAAAA	TTTGAAGGAAACCATCTGGC	60	FP	180	492	AAAAACCAA
Ya5ACA1853	AL355535	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	ATATATTCAA
Ya5ACA1854	AL354855	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	ATGGTGAAACCCCG
Ya5ACA1855	AL391834	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	NONE
Ya5ACA1856	AL513503	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	NONE

(table cont.)

Ya5ACA1857	AL590812	AATGCAAAGGAGGCAGAGTG	CCTTCAAGAATAAGCCACTGA	60	PARA	168	486	AAAAGCAATTAACTTGG
Ya5ACA1858	BX000449	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AAAAGACACAGACTGG
Ya5ACA1859	AL953911	TCCCTTAATCAATCTGACAGCA	TCAGTGCTCTTCGTTCTCCA	55	FP	111	423	ACACAAATT
Ya5ACA1860	AL354874	ATGGAAAAGGGGCTGAGTCT	TTTGTGTTTGGTCCATCAGC	60	FP	105	447	AAGATCTGCTGGCTG
Ya5ACA1861	AL590078	TATTTCCACCAAGAGGGAGC	GGCTCGGTTGGTTGTTTTAG	60	LF	166	481	AAAATGCTTGA
Ya5ACA1862	AL596385	CAGAAGCCCATGAGTCCAAT	TGTGCTTCTCCACTCACAGG	60	FP	118	441	AAAAACCATGCAAGC
Ya5ACA1863	AL162232	TTTAAAACTTGGGTGAAAGG	TGGAAGAAAACCATAGTTCC	55	FP	381	678	AAAAATTT
Ya5ACA1864	AL953911	TGCTGACTTTGCTGTTTACTGG	GGGGCCATCTAAGTTTCACA	60	FP	122	435	AATGGCTTTCT
Ya5ACA1865	AL353729	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AATTAAAAATA
Ya5ACA1866	AL161724	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AAGATTAGACTGCCCT
Ya5ACA1868	AL365502	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	TTATTTT
Ya5ACA1869	AL161457	GTGGAGGAAATTGTCCGAGA	CTCCAGCCTCTGTGTTCCTC	60	FP	188	487	AAAAAGGAGGCATC
Ya5ACA1870	AL162252	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AATAATCC
Ya5ACA1871	AC006450	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AAAACTGGAAAAA
Ya5ACA1872	AL354711	TTCAAGCTGAGGGAGTCA	GTTAAAGCAGCTGAGAGGAA	55	FP	253	572	AGAAGTGTAGATTATTG
Ya5ACA1873	AL354979	AAAACAAAAGCTGAGTGCGG	TGTGTGTTGAGGACTCCCAG	55	FP	147	464	AAAGAGAGGACA
Ya5ACA1874	AL513102	CAGTGATATTTCTCGAGTGCT	AATATTTATGGGCCAATCG	55	FP	65	382	AGAAGGATGCCTGGC
Ya5ACA1876	AL591662	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	TAAAAGTACAAAA
Ya5ACA1877	AL354676	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AAAATCTACCCAGGCTT
Ya5ACA1878	AL133410	AAGGGCAGACATGCCAAATA	TCAGGTCTCTTTCCATCATCTCT	60	IF	174	477	AAATATGTTCAG
Ya5ACA1879	AL158830	ATCCTAGTGCTGAGGGGGTT	ATCCTTTGCCCTAGACAGCA	60	FP	90	395	AAAAACATTTC
Ya5ACA1880	AL451124	TGCTGTGGCTACTGCCATAA	GGGTTCTTAGGTGGATTCAGTG	55	FP	99	402	AAGAATTCAC
Ya5ACA1881	AL359636	GGATTTTGATAAAGCCCCCT	TCAAGAGGCTGAATGTGGTG	55	FP	110	423	AAAGACCATGTATGG
Ya5ACA1882	AL353666	TCCAAATGTTGAACAGGCAG	CATCAGTCACATCCCCTCCT	60	FP	438	755	AATTGCAATATAG
Ya5ACA1883	AL162726	AGGCTGTGAAATGCTCCCTA	TGTAAAAGGCCCAGATCCAA	55	FP	122	428	AAAAAAGGGTTTTCCA
Ya5ACA1884	AL158154	TCACCCGTAAATGGTGACAA	TCAGAGTGCAAGGAGAGCAA	55	FP	136	457	AAGACAAGATGGTG
Ya5ACA1885	AL158047	ATGCTTGAATGATGGTTTGC	CTCTGCACCATCAGGAGGTC	55	FP	123	397	AAAAGTTTGTTTCT
Ya5ACA1886	AL445532	TTGCCTAGCTCAGAACCCAG	ACCTGCAAAAATATGCCCAA	60	FP	210	491	AAAAAATCAGTTGG
Ya5ACA1887	AL390838	TGCCTAGATTTCTGCCTTTCT	TCCAATGCGGTTTTCCTATC	55	FP	102	410	ATTCATTA
Ya5ACA1888	AL158154	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AAAAAGAGAAAGAG
Ya5ACA1890	AL353662	ATGTCCTGCAGACTGAGGGT	TGGCAGTCTGGTGTTGAGTC	60	FP	148	471	AGAACAGTGCC
Ya5ACA1891	AL137022	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AAAAAAACTATGGC
Ya5ACA1892	AL162585	GAGCTCCACACCAAGCTTTC	CAGCAGTGACCTGTTCCTGA	60	FP	181	491	AAGAGCAGGTGGTT
Ya5ACA1893	AL353649	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AAAAAGAAATTCGGAGC

(table cont.)

Ya5ACA1894	AL353748	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AAAAAGACACAGAGGA
Ya5ACA1895	AL136367	CGAACAATTGCACCCACATA	AGCCCTGAAAGGATACACCC	60	FP	97	390	AAATACCTCAAATTG
Ya5ACA1896	AL391219	GTAAGTGGGAACCCTGAGCC	TGTGTTACTGGCTGCAGAAAA	60	FP	169	482	AGATTTCCCATCTTC
Ya5ACA1897	AL445925	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AAAAACCAAAATTG
Ya5ACA1899	AL160269	TCCAGTAAGTTGTGGAAATAAACTG	TTCATTCTGGATGGTGGGAT	60	FP	145	482	AAAAAACCATTTTCC
Ya5ACA1900	AL159167	NOT AMPLIFIABLE	NOT AMPLIFIABLE	-	NA	-	-	AAAAAAATGGG
Ya5ACA1901	AL591502	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AAAAACACACCTCA
Ya5ACA1902	AL161454	TGGGGGAAGGAATATTTGAG	TCATCTGGTTGAAGGAATACCC	60	FP	190	500	AGAAAATGAGG
Ya5ACA1903	AL161728	GAAATAAAAAGGAAGGCAAGGAA	GCCCTTATGGCATTCACAGT	60	FP	96	430	AATGACTATATATA
Ya5ACA1904	AL160269	TGATAGCTACCCTGGGAACG	TTCTCTTTTCTCCATTCAGTTCA	60	FP	170	479	GAAATTTAGTTTTAAC
Ya5ACA1905	AL391867	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AAGAAAAAAAAAGCC
Ya5ACA1906	AL353621	TCCATGTGAGGCAATCAGAA	GCTCCCATTTGCACACTCTT	60	FP	62	369	AGAAACTATCCT
Ya5ACA1907	AL589823	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AAAAGTACCCAGG
Ya5ACA1908	AL359710	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AACTTATGAG
Ya5ACA1909	AL133413	GGAAGGAGGCATGAAACAAA	TCTCAAGCCTGCCATAACAA	60	FP	145	472	AAAATCTTGCTCAG
Ya5ACA1910	AL162415	NOT AMPLIFIABLE	NOT AMPLIFIABLE	-	NA	-	-	AATCTATTCCTTTCTC
Ya5ACA1911	AL360218	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AAAAATTAGTCGGG
Ya5ACA1912	AL392084	GAGGGAAATGTGGTTGGAGA	TGATGATGCTTGTCCTGGAA	60	FP	172	489	AAAAATTCTGCAGCCA
Ya5ACA1913	AL359846	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AAAAAAATCCTCCTT
Ya5ACA1914	AL359846	ATGCCCAGAGTGAACTTGCT	ATTTGGCAATTCCTGGAAGA	60	FP	402	715	AAAAATTTCTC
Ya5ACA1915	AL589844	TCTCTCTTCCATGGATTTTTCTG	TCTCAGAATGAAAGGCTGTTTCT	60	FP	96	424	AAGAAAAAGA
Ya5ACA1916	AL590491	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AAAACATA
Ya5ACA1917	AL358779	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AGAAATTA
Ya5ACA1918	AL135789	NOT AMPLIFIABLE	NOT AMPLIFIABLE	-	NA	-	-	AAAACCAAAGCC
Ya5ACA1919	AL354982	CCCCAAACCTAGCTAGAGCC	TGGATGAAATGGCGTGTCTA	60	FP	121	431	AAAAAAGAACTGGC
Ya5ACA1920	AL449305	NOT AMPLIFIABLE	NOT AMPLIFIABLE	-	NA	-	-	AAGAGCTAGGGAA
Ya5ACA1921	AL133282	NOT AMPLIFIABLE	NOT AMPLIFIABLE	-	NA	-	-	AAAAATGTATTTGA
Ya5ACA1922	AL133284	NOT AMPLIFIABLE	NOT AMPLIFIABLE	-	NA	-	-	AAGAATCATGTGAG
Ya5ACA1923	AL445925	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AAAAACCAAAATTG
Ya5ACA1924	AL591644	CCTTGAATGCCCTTGAATGT	TTGCTTCTCGGAGCAATTTT	55	FP	148	458	AAAAATTGCTCCGAGA
CHROMOSOME 10								
Ya5NBC321	AL121748	GGAGATCCTTCTTTTTCAGCAA	GGAGGTGTCATCCTGGTACA	60	FP	455	145	AAAAGAAATTTCTT
Ya5NBC343	AC005660	GACCACACTGGTCAGGGACT	CCCTCTTTGGTCTTGAGTGG	60	FP	457	154	AAAAAAGCCCTTGCC

(table cont.)

Ya5 415	AF067844	TTTCCAGCATCCACCTCTCT	CCAGGAAATGGGTAGGAACA	60	FP	531	208	CACTCACTTATTTTT
Ya5 521	AC021037	AAGCACATTTCAAACATAACTTGA	CATTTTGGGGTAGTGCTTCAG	60	FP	459	141	TGCAAAACACATTTTT
Ya5 535	AC016396	AGCCATCCTTTCTCCTTGGT	GGCCTCTCCCTACAGTCCTC	55	FP	436	135	GACTATTTTTTT
Ya5 541	AL117336	GGATTGGGAAAGGTGTTGAA	TGGCTGAGAAAACCTGCAAT	55	IF	471	141	TTTTCTCCTTTT
Ya5 554[2]	AL358214	ACTGAAGGAAGGCCAGCAT	TTCTTCTGCCCTGGACAAAC	60	FP	412	79	AAGCT
Ya5AC1925	AC024073	TCGGGGAAAGAGGAAAAGTT	GCAGGAATCCTCTGCTTCAC	60	IF	490	195	TATT
Ya5AC1926	AC036101	TTTTGTGAAGAAGCCCTGGT	GCAGAATAAATGCTGCAACG	60	IF	495	256	AAAACAAGATCTG
Ya5AC1927	AL596113	GGCCAGTGAGGGTGAAGTAA	AATTCCCAGCTTGTGCAGTT	60	FP	498	195	AAAAATCCCCAACTG
Ya5AC1928	AL590636	NOT AMPLIFIABLE	NOT AMPLIFIABLE	-	NA	-	-	AAAACTCATGTAG
Ya5AC1929	AL451164	ACACTGTGTCCCTCCAGCTC	ACACAGGGCTCTCAGAAACG	60	FP	459	146	AAAACTGAAGTTG
Ya5AC1930	AL358033	TATTTCCCAGAGGTTCCGTG	TGCTAACTAAATTTTTGGCCC	60	FP	469	149	AAGAAGGGCCAAAAATT
Ya5AC1931	AL158834	GGTCTTTAGGCATTTGGGGT	CCTCAAAATGTATACTTTGGTTTT	60	FP	328	69	AAAAACAAAGTA
Ya5AC1932	AC036101	NOT AMPLIFIABLE	NOT AMPLIFIABLE	-	NA	-	-	AGAGAGTAAAAATT
Ya5AC1933	AL591408	NOT AMPLIFIABLE	NOT AMPLIFIABLE	-	NA	-	-	AAAAATACAAAATTAGC
Ya5AC1934	AL365210	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AAAGACACACGC
Ya5AC1935	AL390715	TTGGAAAATCCCAGGTAGCA	TGTAAGTGTTCACAGAATAGGAGAA	60	FP	449	178	AAAAACATCTA
Ya5AC1936	AC009144	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AAAAAATTAGTTGGG
Ya5AC1937	AL357520	TGGAAGGTAAACAATGGCAA	GCGGTTAATTATCCAGAGGC	60	FP	475	169	AAAAAAAAAAGAAG
Ya5AC1938	AL512631	TGCCAGTCATTGCTCTAAACA	CCCTTGAAGGCAAAACATTG	60	FP	497	182	AAAAATTGTAG
Ya5AC1939	AL160287	GCCAAAAAGGAAATCACAATG	GTCTCCTATCCCAGCCATGA	60	IF	446	140	AAAAATTGACATATAT
Ya5AC1940	AL158036	GCCTTGCAGAGAGTTTCACC	TCCCCTCATCTCTCTGATGG	60	FP	1188	876	AAAAATACAGATGG
Ya5AC1941	AC092405	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AAAAATTAG
Ya5AC1942	AL158167	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AGAAAAAATAAGGAACT
Ya5AC1943	AL160289	TCCACTAACAGCGGTCAAAA	ATACCTTGGGGAGGACGTTT	60	FP	486	160	GAAAATATGTAGTCT
Ya5AC1944	AC021039	NOT AMPLIFIABLE	NOT AMPLIFIABLE	-	NA	-	-	AAAAGCATCT
Ya5AC1945	AL731534	TGCCTAGTCCTGAATCCACC	TGTCAGATCAGAAGGCGAAG	60	FP	500	183	GAAAGTACTTTAGG
Ya5AC1946	AL445463	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	NONE
Ya5AC1947	AL359697	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AAAGATGTATAAAG
Ya5AC1948	AL355300	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AAAAGACTACACATTGGG
Ya5AC1949	AL450334	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AAAGAGTCTC
Ya5AC1950	AL022344	NOT AMPLIFIABLE	NOT AMPLIFIABLE	-	NA	-	-	AAGACTGCTGA
Ya5AC1951	AL022344	AATAATGCATGGGCCAAAAA	ACTGCTGAGCTGTACCCCAC	60	FP	406	86	GAAAATACAACACGTGA
Ya5AC1952	AL353790	AGCCCCAGATAAACCCACTT	CAAATTTCACATACACAATGCAA	55	IF	483	163	AAAAGATTAGTAAG
Ya5AC1953	AC016745	NOT AMPLIFIABLE	NOT AMPLIFIABLE	-	NA	-	-	GAACATAATGATT

(table cont.)

Ya5AC1954	AC063961	NOT AMPLIFIABLE	NOT AMPLIFIABLE	-	NA	-	-	TATTTTTTG
Ya5AC1955	AL450388	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AAAGAGTCTC
Ya5AC1956	AL117341	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AAGAAACTCTTTTGA
Ya5AC1957	AL589822	TTCACTCTCCTTTTGGGCAG	ACAAACTGGCTCGCTTCTGT	60	FP	1069	744	AAAGAATTAGTAACTTT
Ya5AC1958	AL117341	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	TACA
Ya5AC1959	AC016397	GCATTAAGTGAAAACAAAAATCTG	TGCTCATGATCCAGATAACATCA	55	FP	492	189	AAAAATGTT
Ya5AC1960	AC084727	TGAGATGTGCTGGAGTGTGAG	CAAAAAGGTAAAAAGCAACAGG	55	IF	499	182	ATATC
Ya5AC1961	AL157399	CCTTTTGTTACCAGCACTGATT	GCACAAGCTCACTTCTGGTTC	55	FP	473	162	AAGATAAGATCAG
Ya5AC1962	AL158163	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	NONE
Ya5AC1963	AL159170	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AAAAATTAGT
Ya5AC1964	AL138921	CACATTTCCAGCTTTTGGGT	AAGAAACTGGTCGTGATGGG	60	FP	499	176	AATAAACCCCAT
Ya5AC1965	AL512284	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	GAAAATAAAAAGATA
Ya5AC1966	AL445463	GGTTTTAAATGCCGCTGCTA	TGGTGGCTCGTACAGAAAAA	60	FP	462	145	AAAAAATTAGTTTCT
Ya5AC1967	AC026884	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AAAAAATGATGAGTTC
Ya5AC1968	AL159170	TCCCTCCTTCTGGAAATGTT	CAAAAATTGCAGAGCCATCA	55	FP	500	181	AAAAACTCAATTCTTG
Ya5AC1969	AL445463	TTTTCTTATCAGTTCACCCCTG	TCTGACTTTTTGCTGGCCTT	55	FP	493	175	AAAAACTTGC
Ya5AC1970	AL445463	CCGTTTAAAAGGACCACTGC	CCACCTCCATAGCTACCACTG	55	FP	452	139	AAGACACTACTTC
Ya5AC1971	AL158163	CACCCCATCCAGCTCAATAC	ATGGATGCTTGCTACTTGGG	55	FP	496	186	AAAATTTGC
Ya5AC1972	AC025427	TTGAGTGGAAGGCTTTGTCA	TGACAGTATGGGCGTAGGGT	60	IF	500	167	AACCATGAAATTA
Ya5AC1973	AC023170	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AAAAAGTTATGGT
Ya5AC1974	AL392046	TGTCACTGCAAAGAAGTGGG	TGCTATGAGCATATTTTGGGG	55	FP	1061	744	AAAGAATTGCTACA
Ya5AC1975	AC013287	GCTGCTTAGCATTCTTCCCA	TGGATAATTTCTGTTCCTACTTTCG	60	IF	451	142	AAAACTGTATAAAACG
Ya5AC1976	AC010863	AAGTTTCCTGGCTTGACCCT	TGACAGAAAAATTTGCCCTCT	60	FP	467	143	AAAAAACAAGC
Ya5AC1977	AL590502	TCATGTCTTTCTGCATTTCCA	TTGTTTGGAATACTGCCTGG	60	FP	1197	872	AAAAAGTTTTA
Ya5AC1978	AL603824	TGCATGTCCCATTTGTTCTG	TCCTTTCCCACTCTTCCCTT	55	FP	477	308	AAAAAAAGTGATGAGATG
Ya5AC1979	AC024600	NOT AMPLIFIABLE	NOT AMPLIFIABLE	-	NA	-	-	AAAAAAATCC
Ya5AC1980	AL713888	TACACCCCAAGACACTGGGT	TGCAACTATCTTCATATCCAGGAG	55	IF	1130	808	AAAGATAAATGATA
Ya5AC1981	AL136233	AGTCACTGGCTTCACCCATC	GGGGAAAAATGTTTTGGTG	60	FP	904	596	AAAACATTTTTG
Ya5AC1982	AL390716	GTGTGTGGAGGTGCTTCAGA	GAGTCCTGGAATTCCTGCTG	60	IF	470	148	AAAGAATTCT
Ya5AC1983	AL357520	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AAACCCATGCCA
Ya5AC1984	HSCALM	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AAGAAATATATTTC
Ya5AC1985	AL355344	NOT AMPLIFIABLE	NOT AMPLIFIABLE	-	NA	-	-	ATATTTTTTTC
Ya5AC1986	AL138925	AGCAAAAGGCAGATTCTGGA	AGGCAGTTTAACGTGTGGCT	55	IF	487	176	AAGAGACATCAGGA
Ya5AC1987	AC073370	CAGGAGTTAAGGGCAGGTC	GTCACAGGCATGAGCCACT	60	FP	895	586	AAAAAAATCTA

(table cont.)

Ya5AC1988	AL731563	TGGCAAGTCATCTCTGTCTTTT	TTCCATTTCTCTGATCTACCCAA	55	IF	425	113	AAAAAGCAAATAAA
Ya5AC1990	AC010864	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AAAAAGATGCTC
Ya5AC1991	AL392111	NOT AMPLIFIABLE	NOT AMPLIFIABLE	-	NA	-	-	GAAAAATAAGAATAG
Ya5AC1992	AC013242	NOT AMPLIFIABLE	NOT AMPLIFIABLE	-	NA	-	-	AAAGAGAAAGCACC
Ya5AC1993	AL136982	CACGGGAGAAAACAGAGAGG	GAGTGAAAGATTGATTACGGCA	60	FP	486	166	ACTGA
Ya5AC1994	AC021028	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	GAAAAAATGTTCAGCATC
Ya5AC1995	AL355141	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AAACATACATG
Ya5AC1996	HS1119I23	ATGTAACTCCACCACGGAGC	TTTGCTCATGAGTTTGCAGG	55	FP	1149	831	AAAGAGCCCTCGTGG
Ya5AC1997	AC069540	GTTTGTGCTTCAGTGGCCTT	CAGGTGGCATTACCACTCCT	55	IF	480	159	AAATAAAATCAGCATC
Ya5AC1998	AL356795	TGAGAGCTGCCTAAAATGCC	TCTTCTTCGGCAGAGTGTCTT	60	FP	448	139	AAAAATGTGGAAATG
Ya5AC1999	AC091487	AGTGTTGGGAATGTCCACAG	GCAGATTAGTGAACCCAGCC	60	FP	478	167	AAGAAATCTA
Ya5AC2000	AL139340	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AAAAATTTTTTTTG
Ya5AC2001	AL844892	NOT AMPLIFIABLE	NOT AMPLIFIABLE	-	NA	-	-	TTAGG
Ya5AC2002	AL157389	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AAAGAACTTA
Ya5AC2003	AL356142	NOT AMPLIFIABLE	NOT AMPLIFIABLE	-	NA	-	-	TGATACT
Ya5AC2004	AL359198	GCCATTCCTGTTTTGCAGAT	AAGCAGAAGTGGGAAAGCAA	60	FP	484	173	AAGAAACTTTCCC
Ya5AC2005	AL138759	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AAAAAAAAACTTGC
Ya5AC2006	AL139118	NOT AMPLIFIABLE	NOT AMPLIFIABLE	-	NA	-	-	AAAAGAAATACCGA
Ya5AC2007	AL161652	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AAAAAAATCACAAGA
Ya5AC2008	AL162502	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AACACAATGG
Ya5AC2009	AL138759	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AAAGATTTCTACATG
Ya5AC2010	AC068062	CCTTCTGTTTCTTCTCTTCAGTT	GAGATTAGAGGAAATGATCAGAGC	60	FP	489	144	TAAAAATGCAAGATA
Ya5AC2011	AL138921	NOT AMPLIFIABLE	-	-	NA	-	-	AAATAAATAACTT
CHROMOSOME 11								
Ya5NBC27	AC003691	CTGAATACAGGTATCACTGAACAGAAC	ACAGTGTAAAGTCTAACCTACCAGA	55	IF	591	265	AAAAAAAAGAG
Ya5NBC46	AC009466	GATGTGTGAATACTGTGTAGATTCCAG	GTAAAGCTTTTGTAGTGCCTAGCTC	55	FP	405	94	AAAACTAT
Ya5NBC48	AC002290	ACTGTTAAGATAGTGAATTTTACTGCTCCA	AACTCACACGTGATACAAAATACTC	55	FP	481	176	CAACTTGGTCTT
Ya5NBC89	AC009807	ATCTTCCCGGCATAAACCTC	GAGGCCCAAATTTGCTTACA	55	FP	516	195	AGAAAGTGGAATTACA
Ya5NBC135	U01102	ATTAAGCTCATGGTAACCAGCAC	GACTCTCCTCTCTGGATTAGAAAC	60	LF	436	117	AGAAGTGGCTTCCCC
Ya5NBC330	AL133399	ATGCTGTGGGTTGCTAAGGA	CTGTCCCTTGTTTGGCTTGT	60	FP	402	88	GATGAAGGCTATTTCT
Ya5NBC355	AL078477	CATCTCACTTGAAAGCCCATT	TGTGTCTTAATGACCCTGGAAA	60	FP	802	481	AATTTATTTTTGGC
Ya5 459	AC002402	ACATTCTGTGCCACAAACCA	CAACAGTGGGTCCTTCATCA	60	FP	403	82	AAAGCTGTAGG
Ya5AC2012	AC087653	ACATGAAGCTTGAGGGCATC	GCAAAGGAATGGGTGTGACT	60	FP	1197	876	AATTTATTTTTGG

(table cont.)

Ya5AC2013	AC084859	TGGCAGATTCTGACTGGCTA	CACGTAAGGTGAAAAGGGGA	60	IF	489	212	AAAGAGAACC
Ya5AC2014	AP003531	TCCAAGTCAAGGAGGAGCAT	AGGGCCAGACTTCTTAAGGC	60	FP	908	624	AAAAAAAAGAATA
Ya5AC2015	AC013762	GAGAGGGTACGAGGTGTGGA	GATAAGTTGGGTCGAGGCAG	60	FP	484	168	AAAAGATCTGAGTGGG
Ya5AC2016	AP000484	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AATAAGTTAA
Ya5AC2017	AP000842	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AACTTACACCTACAT
Ya5AC2019	AC068405	AATGGGAAAAATCGGAATGA	TGTTCAAATGCTCCTTATTTGC	60	IF	456	137	AAAAATACTTTGCA
Ya5AC2020	AC112694	CGTGCGCTTACCTCCTACTC	TTGAGAAATGATGGTTGGCA	60	FP	1200	900	AAAACATGCTAGACA
Ya5AC2021	AC022878	NOT AMPLIFIABLE	NOT AMPLIFIABLE	-	NA	-	-	AAGAGTTAGTTTA
Ya5AC2022	AK021479	CACCTTCAGCTGTGAGTGGA	CATGACACACTTGGTTTGGC	60	FP	892	578	AAAAATGGATTACTTGG
Ya5AC2023	AC090469	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AAATGTGAGAG
Ya5AC2024	AP004241	TTTGACGTGAGGAAATGCTG	TTGTGTTGGGATAACTTGATAGGA	60	FP	468	152	AAGAAGTATTGTA
Ya5AC2025	AL158064	NOT AMPLIFIABLE	NOT AMPLIFIABLE	-	NA	-	-	AAAAAAAT
Ya5AC2026	AP003775	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AAAAATTCTC
Ya5AC2027	AK021479	NOT AMPLIFIABLE	NOT AMPLIFIABLE	-	NA	-	-	NONE
Ya5AC2028	AC084243	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AAGAAATAAATTTCTG
Ya5AC2029	AC079064	AAATGGGGCCCTTCTTTCTA	TGAGACTCTGTGCATGAGGG	60	FP	500	196	AAAAACTGGGCAGCA
Ya5AC2030	AP000818	GTGGCACCTACTGGGAAAGA	GCATCCTCCATGCAAAAGAT	60	FP	483	162	AGAAATACCACCAGAG
Ya5AC2031	AC124657	ACCAACCATTATCCCTGCAA	AAACACAGGCTGCATTCACA	60	FP	495	181	AAAGAATTGTTAG
Ya5AC2032	AF205204	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AAAGAAAAATAG
Ya5AC2033	AC124657	AAAGGGGGAAAAAGGAATCA	AGCTGGCTAGGCTGTGTCAT	60	FP	455	148	AAAAAATCCTTACATG
Ya5AC2034	AK021479	NOT AMPLIFIABLE	NOT AMPLIFIABLE	-	NA	-	-	NONE
Ya5AC2035	AC023950	ATGGGGTGACAAGTGCAAAT	CAGTCATTGTCCTCCTGGAAA	60	IF	491	179	AAGATAGTTCCCAGAG
Ya5AC2036	AC079326	TGAAAGACTGCACGGAAGTG	CATGCCTGTGCTTAGGTTGA	60	FP	482	204	AAAAACTTCCA
Ya5AC2037	AK097534	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	TAAAAAATAAGTAGGAG
Ya5AC2038	AP004241	CGCAGCTCAAAATCATCAAA	TATTATTCCCTAGGTGCGGC	60	FP	1088	778	AAATAAAAGAAAGG
Ya5AC2039	HSJ760G15	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AATCAAAAGGATT
Ya5AC2040	AC015691	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AAAAGTGTTCCTATT
Ya5AC2041	AC130307	GAAAAGCTACATGGGGACCA	CCCACTCCCAAGAAAGATGA	60	FP	1131	812	AAAATAATTTTAAAAGTA
Ya5AC2042	AC023943	NOT AMPLIFIABLE	NOT AMPLIFIABLE	-	NA	-	-	NONE
Ya5AC2043	AC021749	TTCTTGGATCCCCTGCTAGA	GAGCAGTAAGTCCAAAGGCG	60	FP	478	161	AAGAATCCTTGTAATTT
Ya5AC2044	AC087378	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AAAATATTTTA
Ya5AC2045	AC021749	GCCACTTATCCGTTTCAGAAGAT	CTATGGCTTTTCCTGAACTTTCC	60	IF	599	264	ATATTACAAATTG
Ya5AC2046	AC091013	GCCCCGAATGTATCCTCTTT	GGTTTAAATTCAGGGCAGCA	60	FP	789	485	NONE
Ya5AC2047	AC087293	NOT AMPLIFIABLE	NOT AMPLIFIABLE	-	NA	-	-	AAAACAGATCAG

(table cont.)

Ya5AC2048	AC129913	AGCCACCCAAATTGCTCTTA	GGGGAGGTACATTTTGATGC	60	FP	484	175	AAAAAATGTGTCCTA
Ya5AC2049	AC079917	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AAAACCTACTATTTA
Ya5AC2050	AC015820	GTGCCAATGTATGCAACAGG	GGGCGTCCTCTCTTATTTCC	60	IF	460	341	AAAACCATGGATGT
Ya5AC2051	AC087521	GACCCATTTTCTTCCCCATT	AGGAAACACTTTCCCTGCAA	60	FP	464	150	AAGAAGTAGACAAAAGT
Ya5AC2052	AC104978	CCTGGTACAGTGCCCAGAAT	TGAAAAAGCCCTGAAGGATG	60	FP	996	679	TAAAATATT
Ya5AC2053	AC068385	AGTGTCCCCTTCCTCCCTTA	GATTTTTCCTTTTGGGTGGG	60	FP	500	173	AAGAACATCCTG
Ya5AC2054	AC135977	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AAAAAAATC
Ya5AC2055	AC113193	TTCCTGCATTCTTTGAGCCT	CTCCCTCCCAAGGATGATTT	60	FP	442	188	GAAAATGTTTCTG
Ya5AC2056	AP001782	ACAGACACTTGGGGCTGAAG	GAGTGTGTAGGGTTGGAGGC	60	FP	469	162	AGAAATGAAGATGA
Ya5AC2057	AP003064	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AAGAACATCATCAGG
Ya5AC2058	AP004247	TGCACCGTGATTGGAAACTA	AAAAGAATAGGACGCGCTGA	60	FP	429	120	AAAGAAATAAAGC
Ya5AC2059	AC027239	NOT AMPLIFIABLE	NOT AMPLIFIABLE	-	NA	-	-	AAAGACACATGC
Ya5AC2060	AP002517	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AAATCTGGGTAGTGTG
Ya5AC2061	AP001803	GCTGAAGACAACTGCACCCT	TCTCAAAGAGCTTCATGAGTCAA	60	FP	491	172	AAAATACAATCCTATG
Ya5AC2062	AP003064	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	NONE
Ya5AC2063	AP003972	NOT AMPLIFIABLE	NOT AMPLIFIABLE	-	NA	-	-	NONE
Ya5AC2064	AP003532	NOT AMPLIFIABLE	NOT AMPLIFIABLE	-	NA	-	-	NONE
Ya5AC2065	AC013762	CCTGCCCTCAGTTTGCTTAG	CAGGGCCCAAGAAAGTATGA	60	FP	475	146	TAAAAATAACTGTA
Ya5AC2066	AC136297	CTAAGCTCCAGAAGCTCCGA	GCACACATGTGACCCTCAAC	60	FP	1049	745	NONE
Ya5AC2067	AP001266	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	NONE
Ya5AC2068	AC116534	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	NONE
Ya5AC2069	AC130310	NOT AMPLIFIABLE	NOT AMPLIFIABLE	-	NA	-	-	AAAAACA
Ya5AC2070	AP004241	TCTTATCCTTCACAATTGCTTCA	TCCCAATGGTAGTGGTGTTTT	55	FP	391	100	TATGA
Ya5AC2071	AP004369	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AATAATATTTTAT
Ya5AC2072	AP000842	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AAAAGTTTGTCAATGTT
Ya5AC2073	LOC340999	GGCATTCTTTTCAAACGTCAA	TTGCAATTCAAGGAAGTTAGGAA	60	FP	461	146	AAAACCTTCTAGCA
Ya5AC2074	AP000486	AGGCTATTAGAATCCCCTGTGAG	CAGACCAATTAAATCAGCGACTC	60	FP	670	350	AAGAAATAAGATT
Ya5AC2075	AP000486	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	GAAAT
Ya5AC2076	AP003086	ATCTGGCGTGGGGTTTTT	TGCACCAAAATCCTGTGAGA	55	FP	486	174	AAAAGAAAATAC
Ya5AC2077	AP002498	ATGGGCCCTACTCTATGCAG	TTGGCATGGGTTTTCAGAAT	60	FP	499	178	AAAATCCTCGTTGGTG
Ya5AC2079	AP002985	TCGAAGCCACAGAACAAATG	CGTCAGAGAGGGGAACTCAC	60	FP	477	181	AAAAAT
Ya5AC2080	AP003531	TCCTTTGCCACACAGTCTTTT	CGATTTCCTGGAGAGGATTTT	60	FP	478	160	AAAAGTTGTTTTCT
Ya5AC2081	AC090538	TGTGAATTCAGCTCAGCAACA	TGGATGGAAACTGACAAGGA	55	FP	493	164	GAAAAATTGATCTTGAATTTT
Ya5AC2082	AP000764	TCGATTCGACATAACTGCCTAAC	GGACACATCTGAGTTAGGAGCAC	60	FP	831	513	AAAGAATCCAGGC

(table cont.)

Ya5AC2083	AP000773	ACAGAAGATGGGTCTGGGCT	AAAACAGTGAGACCGGTTGG	60	FP	912	618	AAAAAAATGCATTCCT
Ya5AC2084	AC022399	TCATGGAGTTGAGGCCTTTT	CACTACCTGGGAGGACCAAA	55	HF	497	180	AAGAACTGGCTC
Ya5AC2085	AP003059	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	TAAAAAGTCTA
Ya5AC2087	AP000974	TTGTGGTCAGTGCTTCGTCT	GGTCTTGTGATTTTAGCCCC	60	FP	500	243	AGAAGTACAATG
Ya5AC2088	AP001528	TTTTGAAGTGCCTGATGCTG	CCAGTTGCTTGGAAACACAA	55	FP	409	138	TGAGT
Ya5AC2089	AL355500	CCACCTGTAGTTTTCTCACTTGT	GGGACATCTCTGTCTTGTTTTTG	60	FP	583	249	TGCAAAATGG
Ya5AC2090	AL355500	ATTTGGTGGTAACACATCCAGTC	ACGGAAGGGTCACATCATTTAG	60	FP	985	663	AAGAAGCAG
Ya5AC2091	AP003093	TCCCACCCCACTACTAACCA	GCAATCAGGAGGTTATTGGG	60	FP	442	164	AAAAAGTATACTTTCT
Ya5AC2092	AP000852	GGCTTCAGGGGGAGTAATGT	CCACACCACTCCCTCATCTT	60	FP	485	171	AAAAGGTTGACTCTC
Ya5AC2093	AP001791	CTTCTGGGCAGTTCTTGAGG	TCAAGGACATATGGGGAACAA	55	FP	1071	302	AAGAACTGAG
Ya5AC2094	AC129913	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AATAGTTATTCTG
Ya5AC2095	AP000648	CTAAAAGGGACACCAGCCCT	TGAGTTATTTCCCCTCTCCG	60	IF	481	142	AGTTTACT
Ya5AC2096	AP002364	AATGCGATCTTGTCAGAGCC	TCTGGGTACTTGGAGTCAGTCA	60	FP	384	60	AAAACATATATCTG
Ya5AC2097	AP001482	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	NONE
Ya5AC2098	AP003386	CTGTTTCGTTGCTCAACCCT	GCGCATGCCTATGAGAATTT	60	FP	835	500	ATAATAATAATCATAAATTAG
Ya5AC2099	AC103681	CTTTTAAGCCCCAGTTTCCC	CAGTGGGTCCTCCAAAGATG	55	FP	488	174	AAAAAGAAGATAATAACT
Ya5AC2100	AP000870	AGCGCTGGATAGGAATAATTAGC	ATGCCTTCCTAATCCCATCTTAG	55	FP			AAAGAATGGCAG
Ya5AC2101	AP003969	AGTGGGGAAAAGATATCGGC	CAGCATTCATCAAAATTGGTC	55	FP	485	174	AAGAAATACATATTTTG
Ya5AC2102	AP003969	CCTGCTATTCCTTTCCTTTAGTG	GTGACTTCTAGCCACAAAAATGG	55	IF			AAACACTAACAGATTTTC
Ya5AC2103	AP003072	TCCAATCCCATTGCTTTCTC	GGATCCCAATTCCAATCTGA	60	FP	1076	769	AGGGC
Ya5AC2104	AC068205	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AAAGAAGTTT
Ya5AC2105	AP002814	TGTGATTTACTTCTTGAGTTTTCCT	AACAGAAATTGAATGGACACCC	60	IF	499	174	AAGAGTTTATTATT
Ya5AC2106	AP000851	GAGAGATTCAGCACTCCGAAA	CAAATGACCACGAAGTGTCG	60	FP	377	61	AAGAATAGCCGA
Ya5AC2107	AP003043	NOT AMPLIFIABLE	NOT AMPLIFIABLE	-	NA	-	-	NONE
Ya5AC2108	AP002829	GCCATTCCTCTTTCCCATTT	TAGCCGATGCTAGGAACACC	60	FP	753	439	AGAAATTCCA
Ya5AC2109	AC090559	CCCACAAGGCCTAGTCAAAA	ACTATGCCTGGGTCAGTTGG	55	FP	487	174	AAAAAAAGATGGCTCAG
Ya5AC2110	AC018531	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AAATGAAGGA
Ya5AC2111	AP003064	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AAGAACATCATCA
Ya5AC2112	AP001001	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AAGAAATATTTTTCC
Ya5AC2113	AP003123	CAACTACACGGCAGCAACAT	CAGGACATCGGTTTTCCAGT	55	FP	397	80	AAATTTTAAGGACTG
Ya5AC2114	AP002453	GAGCAAGGTTGTGCAGGTTT	GCTTTCACTTTAATAACCCATTGAA	60	FP	484	164	AATCAGGATTGTC
Ya5AC2115	AP002453	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AAAAAAAAAAAAGATTTG
Ya5AC2116	AP003173	TGTGCACAAAATGCATCAGA	GTTCAAGCCCCAGGTGTAGA	60	FP	395	91	AATCCAGCATTTT
Ya5AC2117	AP001023	TCTGACAGTCCACTTGCCAT	CTAAGGGCCTGATTCCCAA	60	FP	499	180	AAAAAGGAG

(table cont.)

Ya5AC2118	AP005718	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	NONE
Ya5AC2119	AP002499	TGGACCCTGTGTTCAAAACC	CAAAGGGGCATCTCTCTGAT	60	FP	423	102	NONE
Ya5AC2120	AP004609	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	NONE
Ya5AC2121	AP000826	TGCACAGTGGCACTTTCATT	GTGCTGCTCACAATGTTGCT	60	FP	478	166	AAAATACAATAGCA
Ya5AC2122	AP001994	GATTATTGGGCCAGCTTGAA	GAACAAATTCAGCACGAGCA	60	IF	1123	835	AGAAAGGA
Ya5AC2123	HSM804574	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AAAAATACAAAAAAA
Ya5AC2124	AP000843	TTGAGCAGACTTGCAGTTCC	GACAGAGGTGGGGTAAGCAA	60	FP	454	135	AAAAAAGTCCTTGGTG
CHROMOSOME 12								
Ya5NBC104	AC07065	GGGCATAGCTGTAGATATAAGCACTACAA	AGAAGAATAGAGGACTATGTCTGT	58	FP	508	188	ACTAATTTTT
Ya5NBC114	AC007782	NOT AMPLIFIABLE	-	-	-	-	-	AAGAATATTTACTG
Ya5NBC136	AC008124	CAGCAACAATCAAAGTTTATAATGC	GGAAAATTGAATGATGGCAAA	60	FP	749	439	GAAAAAGATAAGTT
Ya5NBC147	AC007656	TAGCTGGGGGAGGTAGATAATAAAC	AAATATCACCTTATCAGTGGGACCT	60	FP	493	155	GAGCTTGGTGT
Ya5NBC199	AC005293	CTACCATCAATAACTTGGACACAGA	ATTACAGAGAGCCTGCCATGAT	60	FP	500	200	ATGTCTTT
Ya5NBC217	AC007298	NOT AMPLIFIABLE	NOT AMPLIFIABLE	-	NA	-	-	AAGAATCAGCCAGGG
Ya5NBC338	AC009510	TCAAGAAGCTAAAGGCACCAA	AGGGGAAGAGGAAAAGATGC	60	FP	564	271	TAAAATGTAGC
Ya5NBC359	AC007564	GCAAGTCCTATGCAAGGTCAA	AGGCTTTTCAAGCCAGTGTT	60	FP	775	457	AAGAAATAAAGTG
Ya5 490	U63312	CAAGAAGGAGATGAGGAAGCA	GGAGAGGCATGGTGAGTGAT	55	FP	451	134	AAGAAGGAGATGTAGGC
Ya5 511	AC024900	CCCCAGGTGATATAGCTGCTT	CCATTGGACTTGGCAGTTAAA	60	FP	423	98	CACACAAAACTG
Ya5 515	AC026126	CCATATGGTCCACAAAACCA	CGTTCTTGGATGCATTTTTC	55	FP	477	159	TCAAACCCGTAAAGTTTT
Ya5 518[2]	AC020637	GCAGTAAAGGAGCAATTATCACAG	CCGGAATAATGTAAAATCACAGTGC	60	HF	548	228	GACATTTGCTTCTTT
Ya5AC2125	AC023795	TACCAATGTCAAGCAATGCC	TGTTGAGCATGTAACCAGTTGA	60	FP	455	137	AAAAAGAACAGGTAAC
Ya5AC2126	AC090629	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AAGAATACAAAATG
Ya5AC2127	AC048337	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	NONE
Ya5AC2128	AC084291	AGAGAGCTCACAGGCAGGAG	AAATACACGTGCGCTCTTCC	60	FP	429	111	AAGAAGGGGTGACC
Ya5AC2129	AC004765	CTTCCAATGGATAACCACGC	TCTGTGTTGAAATAGGCCTTGA	60	FP	476	161	AAGAGAAGGTACA
Ya5AC2130	AC079456	ATTGCCAGAAGCTTTCGTGT	TTCCCTGAGCATTTACTGGG	55	IF	476	163	AAAAATCCC
Ya5AC2131	AC026333	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	CTCTTTTAGCAATTTT
Ya5AC2132	AC026333	AAGTGCCTCGCCAATAAAAA	GGCAGAACCTCAGCTCAAAC	55	FP	461	110	AAGAATACAGACTA
Ya5AC2133	AC127002	TTTGACCCACCTGAGCTCTT	CTGAGAAGGGGATGTGGAAA	60	FP	920	609	NONE
Ya5AC2134	AC026333	CCCCTAGCTTCTGAGTTCCC	CTAAGGAAAGGAGGGGAGG	60	FP	488	166	AAGAAGGTCTCCTTG
Ya5AC2135	AC023795	AGGGGCTCAGAACACAGAGA	GCTCTGCCTTCCCTCTGTAA	55	FP	405	89	AAGAAAAAGTCATAG
Ya5AC2136	AC090023	GCACATTTTGCTTGAGACCA	CTGTAGAAACCTTGCTGCCA	55	FP	343	82	NONE
Ya5AC2137	AC087258	GGCAATTTTCTATGGCTGGA	GATAGCTCACCAAAGGCTGG	55	FP	478	159	AAAAGAGTAGTGTCTT

(table cont.)

Ya5AC2139	AC016256	AATTCCACCCTCCTGGTTCT	GGATGCTTGGATGAGGATGT	60	FP	480	175	AAAAACTTTCG
Ya5AC2140	AC087260	GAACGTGGAAAACAGATGGG	ATCCCCATGTCACCATCCTA	55	IF	444	131	AAAAGGTAATTATGG
Ya5AC2141	AC087321	TCCAGGGGATTTTATGACCA	CCTTCCTATGCCAGCCAATA	60	FP	472	161	AAAAAGATGGTAATC
Ya5AC2142	AC069208	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AAGAATGTTGA
Ya5AC2143	AC069208	NOT AMPLIFIABLE	NOT AMPLIFIABLE	-	R	-	-	NONE
Ya5AC2144	AC092453	AATATGGATTTTCCAGGGGC	GTACCTGCCCATTTGTGCTT	60	FP	1192	879	AAAAGCAAAAACA
Ya5AC2145	AC010198	AAAACGTCAGAGCAGGGATG	GTTGCCTTTAGGAAGCTACAGA	60	IF	465	135	AAACAAAGCTAAAGCC
Ya5AC2146	AC092110	GCACAACCATGTAAATCATCAGA	TGATAAGCATATGAGCCACCA	60	FP	497	187	AAAAAATAAGGAGTCC
Ya5AC2147	AC090023	TGGGTTTGTGGTAGAAAGGG	GGCACTGGATGCAGCTATTT	60	FP	990	675	AAAAAGATTCATCCT
Ya5AC2148	AC087588	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AAAAAATGTTTATTCT
Ya5AC2149	AC090023	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AAAAAATTTC
Ya5AC2150	AC084358	NOT AMPLIFIABLE	NOT AMPLIFIABLE	-	NA	-	-	AAGAAGGAGATGTAG
Ya5AC2151	AC127897	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AAAAACTGGA
Ya5AC2152	HS15E1	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AATAATTGCCCTCTC
Ya5AC2153	AC087897	AGGGCTAGCTTGGCTTTTTC	CAAAGGCACATCCTGGTAAA	60	FP	432	113	AAAGAATACCATCATT
Ya5AC2154	AC120104	NOT AMPLIFIABLE	NOT AMPLIFIABLE	-	NA	-	-	AAAAACAAGAAAATTAG
Ya5AC2155	AC084877	CATTTGATTTTAATGGTGCTATGTC	CCATGTGCTGGAGAAAAACA	55	FP	469	157	AAAAGTTATTTTAG
Ya5AC2156	AC025253	AACAAGGTGCCCATCAGAAG	CTCCTAGCTTCCCCATTCCT	55	FP	488	222	AGAAGGTTGC
Ya5AC2157	AC010197	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AAATGGTGCTGGG
Ya5AC2158	AC090675	GGGAGGTGAGGTGCGTATTA	AACATGAACAGAGAGGCCATTT	60	FP	459	155	AAAAATTCA
Ya5AC2159	AC107018	GTCTTTAAGCCTCGGTTCCC	GCACAGAATGGGTGGAGATT	60	FP	977	656	AAGAGATGATATTTC
Ya5AC2160	AC079601	TACATCTGCCATCACCGAGA	ACTCCACCTGTCATCCATCC	55	FP	386	76	AAGAAATACTTGT
Ya5AC2161	AC089982	AACGTAGGCAAAACTGCGTTA	CCTGGAGAGGTGTTTTGTGC	60	FP	480	164	AAAAACAACAACCAA
Ya5AC2162	AC069208	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AAGATACAAATGTCC
Ya5AC2163	AC078920	ACACACAAATGAAGGGAGCC	GCTCCACACCAACACGTCTA	60	FP	481	161	GAAAAATAATGC
Ya5AC2164	AC008083	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AAAACCCAATCTCT
Ya5AC2165	AC024257	NOT AMPLIFIABLE	NOT AMPLIFIABLE	-	NA	-	-	AAGAATAGCT
Ya5AC2166	AC004010	CGATCCATCTGGAAGTCTTGA	TGCAGTGAATTTCCCACTCA	60	FP	420	89	AGAATATCCATCT
Ya5AC2167	AC131157	GATTCTGAGGCAAGCAGAGG	AACTGTGGATGTCGGGCTAC	60	FP	488	160	AACAACTACCTACATGC
Ya5AC2168	AC022073	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	TTTGAG
Ya5AC2169	AC079313	GGGCTAGGAGGAAGTGATCC	GTCTGGGGAGGACATCTGAA	60	IF	483	168	AAGGCATAATATCAG
Ya5AC2170	AC073896	TGGTACTAAGCGCCAGTGTG	CCCACCCTTCATTACCTCAA	60	FP	1179	864	AAAAGAAAAATACAG
Ya5AC2171	AC023055	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AAAAAGTTGGAAAAGG
Ya5AC2172	AC068889	CTGCCTAAGTCTTTGTCTTGA	TGGACTCTGAATGGCTTGTG	55	FP	1125	815	AAAAAAATTAG

(table cont.)

Ya5AC2173	AC073611	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	NONE
Ya5AC2174	AC068889	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AGGCTG
Ya5AC2175	AC087588	ATTTGGGGAACATGGAATCA	CTTGACTCCTGCTCCTTTGG	55	FP	465	163	AAGAAGGAATCATG
Ya5AC2176	AC087241	GCTGCGCTAGTTAATGGTCC	GCCTCATGCCATTTTATACC	60	FP	488	176	AAAGGGTACAGGTTAG
Ya5AC2177	AC121760	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	ATATGCTCACC
Ya5AC2178	AC026351	TTTGCAGAAGAGCACATTGG	CATTGCTTTTTAAATGGCCT	55	FP	445	114	AGGCCATTTA
Ya5AC2179	AC069262	NOT AMPLIFIABLE	NOT AMPLIFIABLE	-	NA	-	-	AAAAAATGGAAGTATG
Ya5AC2180	AC090710	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AGAAGTTAGGATAATGG
Ya5AC2181	AC016145	TTAATTTCCTGGCTTTCATGG	TGAAATCATCAAACATGGCG	60	IF	1173	853	GGCACATA
Ya5AC2182	AC087310	GCTTCCCCAGTGAAATGAAA	TCCCTGAGGTCATTATTTCCA	60	IF	498	167	AATATTGTATATGCAC
Ya5AC2184	AC078860	TTCGTTTTGTGAAAGATTGCTT	ATTTATTGAGCCCACAGGCA	60	FP	464	151	AATACTTAAATAGCA
Ya5AC2185	AC073607	NOT AMPLIFIABLE	NOT AMPLIFIABLE	-	NA	-	-	AAAATGAGATATTAA
Ya5AC2186	AC117503	ATTTGGTTTCAGGGATGCAA	GGACCAAAGAGGCTGAAGAG	55	FP	477	169	AAAAAGCTACTGGTG
Ya5AC2187	AC087897	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AATAATGTTAGCTTTG
Ya5AC2188	AC092747	TTGGACTTCAATCTTTGTATCTTTG	TCCTCCCACTTCTCCATCTG	55	FP	462	145	AAAAAGTTTCT
Ya5AC2189	AC090109	NOT AMPLIFIABLE	NOT AMPLIFIABLE	-	NA	-	-	AAAATGATAATCTG
Ya5AC2190	AC121761	CTTATAGGCCCACAACCCCT	CCTCTCACCCTCTTGACAGC	60	FP	471	184	AAAATAAAGCTG
Ya5AC2191	AC128678	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	NONE
Ya5AC2192	AC092882	GGAACGGGTGACACAAAACT	TCAGAAGGGAGAAAAATCCTTT	60	FP	499	185	AAAGAAAGAGTTG
Ya5AC2193	AC068797	TCCATCCAACAAATCCCATA	TGTTGGTCTGACACCAGTTTTT	60	FP	500	274	AAAAAGCTAAATGT
Ya5AC2194	AC090015	TTGATTTTGAGCTTGTGTTTTGA	AAAAATGGGGCTGTCATAGAA	60	FP	479	161	AAAGATAAAAGAATCG
Ya5AC2195	AC120104	NOT AMPLIFIABLE	NOT AMPLIFIABLE	-	R	-	-	NONE
Ya5AC2196	AC073571	TCACTACTCCGGATGCTCAA	TTGCACAAGAAATGTAGCCAA	55	FP	427	119	AAAATTCACCTGT
Ya5AC2197	AC087600	CCACCTTTGTGCAAAACACA	TTGTTTGCTGAAGCCAAATG	55	FP	413	99	GTCACTGCTC
Ya5AC2198	AC079363	TTCAAGAACATGTAGGCATTTTG	TTCGTTGTCTATTGACATTGGC	55	FP	484	160	AGAGAGTATGTTGA
Ya5AC2199	AC074031	TTCAACTTCTGCCACACTGG	CCAGTGCCTAAAACAGTGCC	60	FP	475	159	AACAATTGAG
Ya5AC2200	AC083812	TTGAAAAGGGAAGCATCAAA	GGAAACATTTAAAGCAAAGTCG	60	FP	479	203	AAAATGCTAAATAA
Ya5AC2201	AC079363	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	GAAAATTTATGACAAAACA
Ya5AC2202	AC073571	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AAAAGAGTGGAAAGAG
Ya5AC2203	AC068798	TGACTATTATTCTGAATGGCCTAGC	AAATGCAATGCTAATGGTTTCTC	60	FP	479	159	AATGA
Ya5AC2204	AC073616	CCCTCTCCTCCACAGGACTT	ATAGTTGGACCCCAGAACCC	55	FP	392	61	CACTATGTTTA
Ya5AC2205	AC073528	CATTTGCACTCAAGTCCTTCAT	TATTTTCCCAAGCGCAGTTC	60	IF	494	171	AAAAATATTAAATAT
Ya5AC2206	AC087600	AAATGTTGGAAAGCCACCAG	AGACTGCCAAGCAGTTTTCC	60	FP	422	84	AAATGAAAAATAG
Ya5AC2207	AC025157	ACCCAAAAAGAAAAACAAAGG	GGGAAATATGGCAAGCTGAA	60	FP	482	155	AACACTCAT

(table cont.)

Ya5AC2208	AC090667	CCCATCTTCCCTGTTCTTCA	TCATCACCTAGCACACGCTC	60	FP	910	588	AAAAATGCAAAAAATC
Ya5AC2209	AC093025	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AAAAAAAACAAATTT
Ya5AC2210	AC133794	NOT AMPLIFIABLE	NOT AMPLIFIABLE	-	NA	-	-	TAAAAATATATGCT
Ya5AC2211	AC090667	ATCAACAGTACCCGAAGGCT	TCACCTTTTCCCACGTTACC	60	FP	393	85	ATCTT
Ya5AC2212	AC018922	GTCAAAACTTTTAAGAATTGGCA	TTTATTTTGTGTCATCTTTCTGACG	60	FP	493	201	AAGAATTGGCAAAACTG
Ya5AC2213	AC087865	AGGGGGAAGACATGAAAACA	AACCACTGAGGACCTGAACC	60	FP	487	176	AAAAATATTTTCCT
Ya5AC2214	AC120105	GCACACCAAAACAAGGGACT	AATGGGGCTTGAGTGTTGTC	60	FP	492	168	GAAATCAACTTGACTG
Ya5AC2215	AC026307	TCACATTCTGCCAGTGTTCC	CAACAATTCCTTGGTCCCTT	60	LF	424	124	AAAAAT
Ya5AC2216	AC090642	GAGCGACAAAAATCGGACTC	GGATGACACCCAAAATCCTG	60	FP	489	163	AATAAAAAGCA
Ya5AC2217	AC009522	GGTTGCCTGCCACATTAAAA	AGCTGTGGCTCTTCCAGTGT	60	FP	427	122	AAAAGTATTGACAG
Ya5AC2218	AC087887	NOT AMPLIFIABLE	NOT AMPLIFIABLE	-	NA	-	-	GAAATAATAGCATT
Ya5AC2219	AC083813	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AAAAATGCACTCATCG
Ya5AC2220	AC125611	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AAAAATAGAGAAGTGTG
Ya5AC2221	AC025164	ACAGCGGGTAGGGAAACTCT	TGGCTACATATGGGATGTGG	60	HF	472	154	AAGAGTTGGATC
Ya5AC2222	AC073655	GTGTTAAGAGGCTGACCCCA	GGATGGGTGGAAAAGAGGTA	60	IF	499	176	AAGAAACTGCTGTTTG
Ya5AC2223	AC090041	CATTGTTGTGTCCCAAGCAC	GCTTAACCTGCCCCTCTTCT	60	FP	1039	708	AGAAATTTAAGTTGAATTA
Ya5AC2224	AC009779	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AAAAATACAAAAATTAG
Ya5AC2225	AC084879	CACAACCTTGGGATAACCCTT	TCATGAGGCGAATGATATGG	60	FP	471	143	AAAACTGAGGTGGCC
Ya5AC2226	AC018474	ATGCCACTGGGAAATTCTTG	AAATGAAGACGCACAGGACC	60	FP	465	163	AAGAAAGATA
Ya5AC2227	AC011598	AATTTCCCCAGACATAGCCC	TGAGAAGCAAACTGTAAGCCAA	60	IF	1150	840	AAAATTGTTGCC
Ya5AC2228	AC007437	NOT AMPLIFIABLE	NOT AMPLIFIABLE	-	NA	-	-	AAGAATTAAAGACTTTC
Ya5AC2229	AC117494	NOT AMPLIFIABLE	NOT AMPLIFIABLE	-	NA	-	-	AAAAAGGTGACCCTG
Ya5AC2230	AC126474	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AAAAAGAGGAAATT
Ya5AC2231	AC063948	TGACAAGTCTTAGCTTTGGGG	CATAGTAGGAATACGGGTGATTTT	60	FP	495	182	ATAAAAAGTAATATA
Ya5AC2232	AC125628	TTTTTCCTCCCTTGGATGTG	TGGAGGGTAAATCCAGTGCT	60	FP	487	202	AGAAAAGCTCCAGAAAA
Ya5AC2234	AC068889	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AAAAGAAGATATGCAGCC
Ya5AC2235	AC079174	GCAGATCCAGGGGATAGTGA	AACTAAAAATGTCAGCCAGGGA	60	FP	369	66	NONE
Ya5AC2236	AC012386	CTTCCTGAGGTTCATTCACATTC	AATTATGGGCATCGTTGAGA	55	FP	668	335	AAGAAATGGGGG
Ya5AC2237	AC005907	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AAGAAATGATGTAATGC
Ya5AC2238	AC004086	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	NONE
Ya5AC2239	AC002395	CACACAGAACATGCCAGCTT	ATGCTATACAGGGCCCTTCC	60	FP	419	109	AACATTGGGAAATA
Ya5AC2240	AC009260	GAAATTTCACCCAGTTGACCA	GCCTCACCATCTTCGACATT	60	FP	483	157	AAAAGTGGATGAAG
Ya5AC2241	AC135251	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AGAAGAGATAATTAGT

(table cont.)

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Ya5NBC176	Z74739	GGGGGAGTATGGTTTGATATACAG	CCCTCATGGGAGGTGTTATTT	55	FP	666	298	AAAAGTTGGTTTCCG
Ya5 481	U67218	ATAGAACCCCTAGATGGGAAAT	TGTCCTAGTAGGGATGAAATATTGG	55	FP	491	178	AAAATTATTCCC
Ya5 544[2]	AL354891	CATGTTCACATTTTGCTTGTTTT	TACCCTCAAGGCTGAACAGG	55	FP	417	123	NONE
Ya5 545	AL354891	AACTGATTTGCCGCTTTGTT	CAGGGGTACACTTATTCCCAAG	55	IF	415	110	GAATGAATGAC
Ya5 549	AL157694	CACAACGGCAAATAGCTGAA	CACAACGGCAAATAGCTGAA	55	FP	474	158	CGAGAGGCGTTTTCTTT
Ya5 552[2]	AL359012	TCAAAGTTCATTGGAACCAAAA	GCAGGCAACTTCAACAGCTT	55	LF	423	131	AAAAGGGTTT
Ya5 555[2]	AL137000	TGCTCTTATGTGGGGAAAAGA	TGGAAAGTTGTGAGGAGCATT	55	FP	424	107	GTTACGGA
Ya5 560[2]	AL159152	TTCTACAACGTGGCCTGATG	AGGGATTGGGAGATGCAGA	60	FP	444	150	NONE
Ya5 568[2]	AL136999	TCACACCAATTTCTTAACACCAA	TTCAGTTGTTACCTAGCCATTTCA	60	FP	548	225	TAACACTTTTAT
Ya5AC2242	AL359831	TTGGATTTATTTCAGCCTACCTG	ATGGGGAGAGGGTTATGTCC	60	FP	407	94	AAGAATGCCCTTG
Ya5AC2243	AL139324	AGCTCCACTGCTATCAAACCA	CGTGTCTAAAGAAGGGGCTC	60	FP	416	97	AATAAGAATCAT
Ya5AC2244	AL158194	GGCTGGTGGCTTCCATACTA	CATTTTGGTGCTGGGAAGAT	60	FP	485	169	AAGAATGGCAA
Ya5AC2245	AL139802	TACATTCCCATGCCTTGACA	GATGGTTGTGGAAGCTGGAT	60	FP	467	155	AAAGAGTACTTTGG
Ya5AC2246	AL512655	TCCATGTAAACACAGACCCG	TTTGGGAGATTTAAAGGGGA	60	FP	491	175	AAAAATACTCTCTCTT
Ya5AC2247	AL157760	TAAGCTTCTGAAGGGCAGGA	GTTTTTATTTCCATTTAGATAGCCA	60	IF	484	166	AAAAAGTTGGCTATCT
Ya5AC2248	AL583848	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AAAAGAAATGAACATTTGAG
Ya5AC2249	AL137248	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AAAGAAATGA
Ya5AC2250	AC012516	CATGGCAGAGGGAAACCTAA	TGATCTCAGCTGCCCTTTTT	60	FP	496	319	AAAAGGTGACCTC
Ya5AC2251	AE014306	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AAAAAAAGAATAACCCAA
Ya5AC2252	AL160158	CCAGCTGAGGTCTAACAGGC	TGCCCTATTTACATTGCACG	60	FP	1018	698	TAAAATAAAAGGTGAGT
Ya5AC2253	AL359920	TCATATGGCAACCAAGGTGA	AGGGGAAGGTGAGTAGGGAA	60	FP	478	166	AAAAGACCAAAGC
Ya5AC2254	AL391873	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AGAAATTTCTCCCG
Ya5AC2255	AL136221	GGGGAGAGATGGCTTCCTAC	TCTTCTCCCCATGTCCTCAC	60	FP	1092	768	AAAAAATAAAAAATAA
Ya5AC2256	AL359538	AATCCCCTACACAAGTCCCC	AGGTGAAACAGCCATTGGAA	60	FP	1074	772	TTTTTCC
Ya5AC2257	AL512655	TTGGGAGAAATAGAAATGTTGC	AAATTCTGCACGCATAAAATG	60	FP	457	136	AGAACATAATGATT
Ya5AC2258	AL160255	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AGAAAACCAAACACAG
Ya5AC2259	AL512484	CCCGAAGTGCTCCATTAGAA	CCATGCATAATGTTCAGGGC	60	IF	383	75	AAAAAAAAAAAGA
Ya5AC2260	AL137142	AAAGGCAGTTCTGGCTGTTG	AGGAAAGGGGAAATGAAGGA	60	FP	478	276	GAAAGTAACT
Ya5AC2261	AL512484	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AAAAGAAACTACC
Ya5AC2262	AL159161	TTTGGTTACACAAGTCTGGCA	TTCCTGGTAGTTGGTTGGCT	60	FP	500	184	AAAATTTGCTATTGG
Ya5AC2263	AL138958	TGGAATGCTGTGTTCCTCAG	AAGGCAGGACCTGGGTATCT	60	FP	1178	863	AAAAAGAAGAACCAC
Ya5AC2264	AL355984	CTTCCCAGGCATTGTGCTAT	ATGTGCTCAATTTCCTTCCG	60	FP	409	90	AGAATGTGGCTATATAG
Ya5AC2265	AE014305	GGTGCCGAGCCTTATCATTA	TGTTTTCTGTTCCCCCAGAC	60	IF	382	63	AAGAAACTG

(table cont.)

Ya5AC2266	AL356961	TTTTAGTTTTGGATTCTTGCCA	ATTCCCAGCACAGGAAATCA	60	FP	1174	889	NONE
Ya5AC2267	AL390029	CCGTGGTCTGTTCATTTGTG	GACCCTGAGAAAGGTCCTCC	60	FP	433	116	AAAACCTCGGAGAAG
Ya5AC2268	AL138681	GGGCCTGTGGTCAAACTACT	CAGTTCTGCTGCATTCTACCA	60	IF	487	152	AAAAATGAGGGT
Ya5AC2269	AL159977	NOT AMPLIFIABLE	NOT AMPLIFIABLE	-	NA	-	-	AAGAAATGAG
Ya5AC2270	AL391600	CCCAAGTTATGCTTTCCAGC	GGCTGTGATTCATTTCCACC	60	FP	1059	743	AAGAATGGATATATAG
Ya5AC2271	AL359763	TCATCCTTCCCCAAGTCATC	CTGGCCATCAACTCTAGGGA	60	FP	455	134	AAAAGTGTTCACTATT
Ya5AC2272	AL136963	GCCCAAAGGGGTGAAATAAT	TTTGGATGCAACAAGTCTGAA	60	IF	464	150	AAAATAAAGAACA
Ya5AC2273	AL139384	CCATTTAAGCCACAAGCACA	TTTGTGAGCTGTGAAGTGCC	60	FP	125	829	NONE
Ya5AC2274	AL356750	GGAAGAACTTTTGCTTTTATTCAA	TGGATCTCTTGCATTTCTGTATTT	60	FP	1200	887	AAAGAATTTATACTGGC
Ya5AC2275	AC129351	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AGAAGTGAGCGAGGGA
Ya5AC2276	AL512642	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AAAGAAAACACATAG
Ya5AC2277	AL162713	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AAAGATATAAAATATA
Ya5AC2278	AL162713	CCACCTGTGGGCATCTAAGT	GGGCACCTCCTCTCTCTTTC	60	IF	477	132	AAAAATGGGATAAATG
Ya5AC2279	AL354816	TCTGGGAATAAAAAGGCAAAAA	CAAGGGTTCTTCAGAGCAGAG	60	FP	454	144	AAAAAAATACAATATA
Ya5AC2280	AL139322	GGGGAGTTTTGAGGTGTGAA	GCTCTGGACAATGTTTTAAGTGC	60	FP	383	60	AAATAAAGCACTTA
Ya5AC2281	AL138963	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	ACACAA
Ya5AC2282	AL139182	GCTGTTATATGAAGTGTTCACCTTG	TGGAAAGCAGAGAAATGCTG	60	IF	498	167	TAAAAATAAAAAA
Ya5AC2283	AL590811	NOT AMPLIFIABLE	NOT AMPLIFIABLE	-	NA	-	-	AATTTTCCAG
Ya5AC2284	AL158196	TCAAGCTAAGGAAGGCCAGA	CTGGAAGGGAAATGCTCCTA	60	FP	436	127	AGGAG
Ya5AC2285	AL136525	TGAAAAATGTGTTTGGCATGT	CAACTACACTCCCATTTTCCTG	60	FP	486	166	AATATTTTGTC
Ya5AC2286	AL390722	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AAAATTCATATGAAAATA
Ya5AC2287	AL356120	CGGAACAAGTTTTCTGCCAT	AAGCATTACTCGCACGAAGG	60	FP	473	152	AAGAATACCTATGAGGAG
Ya5AC2288	AL139081	GTGCTGCTTGCTTGCTGATA	CCAGTGTCTGGAGAGTGGTG	60	FP	487	178	AATAATAACAGCAG
Ya5AC2289	AL137881	GGAATGGGCCCTATAAGGAG	AAAAAGAGAGTGGCCAAGCA	60	FP	464	146	AAGAATGCACTAGA
Ya5AC2290	AL136525	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AAAAATCAACAAGTG
Ya5AC2291	AL161719	TTAAAGCGCCAAAAGGCTTA	GCTTCTGACTGGGGATGAAG	60	FP	474	155	AAAAATTGGAG
Ya5AC2292	AL354798	CAGTATTTAAGAGAGCTTGCTGG	GTTTCAGCCGAAAGCAATTC	60	FP	454	144	CTTGCT
Ya5AC2293	AL359920	AAGAAAGTGCCTGCCACAAT	CATGTCTTGTGCTCTTTGGC	60	FP	1163	857	AAAAAGCAAACA
Ya5AC2294	AE014308	CGACTCTGGTGGAGAAAAGC	TGTTGCCAGACCTTGTATGC	60	IF	464	150	AAAAGATCTTG
Ya5AC2295	AE014305	TGTCAGCAAGAGCTGGACAT	GAGCATCAGAGGGGTGTTGT	60	FP	487	183	AAAGAACAGTTCTG
Ya5AC2296	AL445238	GAGAAGTCTCACCAGGGCAG	TCAATGTAACCGTGTTCCCA	60	IF	955	641	AAAAGAAAATAACA
Ya5AC2297	AE014314	ATACAGCTATTGGCGGTTGC	ACACACAACAGCACATGTCAA	60	FP	499	175	AAAATATGAATACA
Ya5AC2298	AL356750	ACATTCTGTGCCACAAACCA	AGCAACAACAGTGGGTCCTT	60	FP	408	87	AAGATTTAATTCA
Ya5AC2299	AL592490	CAATGGCAGTTTTGCAGTGA	ATCAGAATGCCTTCACACCC	60	FP	499	176	ATTAGACATCA

(table cont.)

Ya5AC2300	AL592490	AAGCTCCAAAGCAAGCACTA	TGTTTCTTAAGGGGGAAGCC	60	IF	489	206	AAAAAAGGAATG
Ya5AC2301	AE014305	CTCTAAGATGGCCCCAGTGA	AAAGACCATGGAACAGGCAG	60	FP	1161	840	GAAATGATAAATCTT
Ya5AC2302	AL355516	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AAAAGAGTTGACTGTA
Ya5AC2303	AL159156	TGCTGGCTGTGTTCAACTTC	TTTTTCCCTGTTTCCTGGAG	60	FP	491	182	AATATTATAC
Ya5AC2304	AL159156	TTGTTGGAAAGAAACCTGAACA	TGCACCGTGGTTGAAAAGTA	60	FP	391	78	AAAGAATTGTA
Ya5AC2305	AL158194	TTCTGAGTTGGTGACACTCCA	CTTACCCAGGCATCCTTTGA	60	IF	398	76	AAGAGTTGTAAT
Ya5AC2306	AL158194	GTGCAGTGCTTGACTGTGGT	GGGCATCAGGCTCATCTTT	60	FP	494	176	AAAAGTAAAAGTCTG
Ya5AC2307	AL596106	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AAGATAGAAAATC
Ya5AC2308	AL353896	GTGGAGGTAGGACCAAATGC	CACCGTCATTAAGCTGAGCA	60	FP	435	140	AAGGAAAAGTG
Ya5AC2309	AL354720	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	ATATATTCTGG
Ya5AC2310	AL355478	NOT AMPLIFIABLE	NOT AMPLIFIABLE	-	NA	-	-	AAGACTATTACAAGGTG
Ya5AC2311	AL445264	TGGTCTACAGCAGCACAAGG	TGCCTTCCCTAGGGTTTCTT	60	FP	496	198	AAAAAAATCC
Ya5AC2312	AL355478	GGCTGGATAGATAACAGGCAA	GGCTTACCACACAAGCCATT	60	LF	484	189	AAGTT
Ya5AC2313	AL161714	TATTGATGCCAGAGGAAGCC	GCAAAATGGAGAGATACTCAGG	60	FP	401	82	AAGAATCAGGTAGTG
Ya5AC2314	AL445929	TGGTCGGATGAATCATGGTC	GAATCCATCATGTAAGGAGC	60	FP	1199	883	AAAGAAAA
Ya5AC2315	AL356416	NOT AMPLIFIABLE	NOT AMPLIFIABLE	-	NA	-	-	AACAAGATAG
Ya5AC2316	AL137140	NOT AMPLIFIABLE	NOT AMPLIFIABLE	-	NA	-	-	AAAAAAGCTAAAGT
Ya5AC2317	AL159154	TCAGAGTCTTTCTGCATCCAA	GGCCTTTTCTTTAAGGCTGC	60	FP	497	200	TCAT
Ya5AC2318	AL445209	CCATAGTTTAGTAGGACAAGCTGGA	GGCTTAAGCAGGTGTCAAACA	60	FP	457	144	AAAGAATACT
Ya5AC2319	AL354806	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AAAGAAGTTGGTGAGCTGA
Ya5AC2320	AL391355	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AATAATTAAATTTTC
Ya5AC2321	AL354852	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AAAAATTAAAAATA
Ya5AC2322	AL161892	NOT AMPLIFIABLE	NOT AMPLIFIABLE	-	NA	-	-	AAATGTGATG
Ya5AC2323	AL355603	CACCCATGTGTCCTTGAAAA	CCATGGATTTTCTGTTTCTGTG	60	IF	413	97	AAAAACTCAATCAGA
Ya5AC2324	AL391995	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	ATCAATTCAT
Ya5AC2325	AL391601	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AAACTGGA
Ya5AC2326	AL158064	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AAAAAAAT
Ya5AC2327	AL445209	GAAATATGCAAATTCCAGAAGAC	TGGGAGCTTAAACACCAAGG	60	FP	435	120	AGAATTTTAAAATG
Ya5AC2328	AC069164	TGCCAATTTTGGTCTGATCC	TCCATTAGCTCCAAAGTCAGG	60	FP	438	103	AAAATCTAACCTGAC
Ya5AC2329	AL445604	CATTGAGGCACCGCATATTA	TGGAACATTTGCTCATAGTCTCA	60	FP	468	145	GAAAAGAAAGTTTGA
Ya5AC2330	AL355481	TTCACAATGCAAGATAAGAAAAAGA	TGACTGGTAAGTATGGCAAGGTT	60	IF	430	112	AAGAAAAAGATTAGTGAC
Ya5AC2331	AL160154	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AAGAGAGTGGATA
Ya5AC2332	AL445604	AAACAAGAGCAAACCAACCA	TTCTGATTGCGTTAATTTGGA	60	-	500	190	AAAAGAATAAACAT
Ya5AC2333	AL590287	TTAATGGAGCATCGGAGACC	ATTCTGCTTTGGCACTTTGC	60	IF	471	166	AAAAAAGC

(table cont.)

Ya5AC2334	AL355580	TGAGGGGAATGAACTTTGTCT	AATCCAGAGAGGAGATGCACA	60	FP	1184	865	AAAAGATAATTTAGTG
Ya5AC2335	AL445647	GACCACCCAGGCATTTAAGA	CCAACTAGTTCCCTTTGGCA	60	FP	457	143	AAGATTGTCTTAATT
Ya5AC2336	AL355677	GTATCACATGAGGTGCCTTGATT	GTCCTTTCCCTAATTCTAATGTCTG	60	LF	585	250	AGAAAAATACTAG
Ya5AC2337	AL445242	CTCCAGTCAAGTAAAGGATTCCA	CAGATAGAGATTTGTTGGCACAAG	55	FP	636	320	AAGAATGATTTATT
Ya5AC2338	AL139798	CCCAAATCTGAAGGCAGTGT	TGTGCAATATCAAAGCCTCA	60	FP	473	169	AGAATG
Ya5AC2339	AC027139	TTTCCACACGGGTTTCTTTC	GTGCAATACAGCTGGAGCAA	60	FP	1139	826	AAAACATA
Ya5AC2340	HS21C002	TTGTTGGAAAGAAACCTGAACA	AAGAGTGCACTGTGGTTGAAAA	60	FP	398	83	NONE
Ya5AC2341	AC026756	TTGGCCCTATATCCAGTACAGAC	AATCTGGACCTAGGGTAAAACTG	60	FP	475	138	AATAATTTGG
Ya5AC2342	AL442067	TTTCCCATGTTGTGTCTGGA	GGCAGGAGGTCAGTCAGAAG	60	FP	1002	687	AAGAAGCAATGTT
Ya5AC2343	AL356580	CCACAATCAAGATGCTGTCACTA	GGTACTTCTTTGCTTTTGTAACCTG	60	FP	585	261	AGAAGTTACCCTA
Ya5AC2344	AL355338	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AAAAGACTGGCA
Ya5AC2345	AL136300	TGCAACCTTCCAAGGACTTT	CTGGCAAACTCATCTCCAC	60	FP	731	410	AATCCCAGCACTTTG
Ya5AC2346	AL445223	AGGGATGGGTGTAGCTCAGA	TTTTGTGTTAGCGATGCTGG	60	FP	475	159	AAATTCAGGAAGG
Ya5AC2347	AL390964	GAACAAGCTCCCTCTGTGCT	GGTCCCTGCTTTATGTCGAA	60	FP	391	83	AAAAAAAAAATACAGTTC
Ya5AC2348	AL590076	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AAAGATTTA

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Ya5NBC39	AC005533	TGGGACTTAGCTGTTTTGGTATCTA	CTAAACACAGGTTACAGCACCTCTT	60	FP	469	152	CTGAAGGAACTTTT
Ya5NBC56	AL109767	TCATTGTATCATCTGCTGTACCTGT	AGTCCAACATAGATGTAATTGGAGT	60	FP	469	148	TTCAAGCAT
Ya5NBC178	AC004900	AGAGCCTGGACTCTGATGTTAGAC	GAGCCATGATAGGAGGAATACT	60	FP	583	260	AAAACAGGAATGC
Ya5NBC303	AL0136295	CTCCTCAAGGTCCCATGTTC	GGTGCCTCTGGGAATGAGTA	62	FP	426	111	GAGAATGAAGTGC
Ya5NBC304	AL132642	GAGCTACTGGCACCTTCCAC	TTTTGACTCACCCTGCTTTTT	60	FP	368	60	AAGATTGCTCTG
Ya5NBC310	AC008372	ATTGCAAATTGGCGATGTTC	CACCACTGAAGCATGCTAGG	62	FP	535	207	AATTAGGTGC
Ya5NBC317	AL132985	CCAAGTCAGGCCACCAATAG	GATGGATAACCTTTTTCCTGGT	60	FP	384	64	AAAAGCTTTGTGAA
Ya5NBC322	AL132800	AGTGCGTCAGATCCTGTTCA	GGGTCTTTGAAAAGTTCATGG	60	FP	451	129	NONE
Ya5NBC333	AL117356	GGCATGCTATCATTCCCAAA	CCAAACTTCTGTTTGAGAGAATACG	60	IF	588	281	CTAAAAGTATTATTT
Ya5NBC334	AL132708	ACACTGTCTTGGAGGCATTC	CCTCCATCCCAGTACCATGA	60	FP	435	117	AGAAAGGGAAATTCTG
Ya5NBC340	AL109985	TCCATATCCCTTGTCTGGTTC	CCTGACCAGGTCCAAATGAC	60	FP	468	145	AAAATACGTAGCATAG
Ya5 419	AC004816	CCACCCCCACTCAAATTCTA	TCCATCACATTTTCCAGCAA	60	FP	422	110	AAAACTTTTGG
Ya5 427	AC005157	CCCTTTTTCACAGTTGCGTA	GGAAACTTGGTATGCTTTTGC	60	FP	409	98	TGAACAAAGGGTTCT
Ya5 486	U67213	CATGGCCAAAGTCCATTAAA	TGAAATCTCCTTGAAAAAGATGG	55	FP	437	122	AAAAATCATGA
Ya5 494	AC022404	GCACTATTACAGCAAGCCACA	CGTTTCCGAATGTGAGATCC	55	FP	459	137	ACTAAAGCA
Ya5 510[2]	AC004900	ACACAACGTGGCAGTTCAGA	GCCTGATCCTGGATAGATGG	55	FP	619	230	AAAACAGGAATG
Ya5 533	AF232289	TGTCATTTTGCCGAGAGATG	TTCCTTCCTACCAATAACCAGA	60	LF	408	125	AAATCT

(table cont.)

Ya5 571[2]	AL356596	AAAGGAGATGGAAAAGGACAGA	TGCAGGTAAATTGCAAGAACA	60	FP	486	122	GGGTTATAT
Ya5JW572	AL161663	CTCAAGACCAGTTCCTACCTGAA	GAGCTTCAAGCATCTCAAGGTTA	60	FP	459	134	AAGAGGGGCTTTC
Ya5JW573	AL139785	GCTTGCTCATGCTATTCCTTTT	CTGGCATGTTTGTTGAATGAGT	60	FP	570	291	CATAACTT
Ya5JW576	AL359238	AATAAAGAAATGGGGAATCCTCTC	GTAGAGATGCGGTACTTTACATTTT	60	FP	501	189	AAAAGCTCCAGTTA
Ya5JW577	AL359238	CTCTGAGTACACACGTTGTCAGC	AACATCCCCAGGTTTTAAGAGA	60	FP	490	182	NONE
Ya5JW578	AL358338	GGTGATCAAATTAACATCCTCAGTG	CTTGCCCAGAATACCACAAAAGT	60	FP	429	106	CCACATCTGGTACTCTT
Ya5JW579	AL358337	TCCAAAGTTGAGTAGGATTGAGC	CTTTTTCTTCCAAGCAAACTGC	60	FP	500	178	GAAAAGTGAGCTA
Ya5JW580	AL356799	GCAACTCAGAGACTTTACTGTGC	TCCACTTTCACTCTCTGGACATT	55	IF	424	144	AGTAATCAACTTCTT
Ya5JW581	AL355112	AATCAAGTGACATCATGCCTAGC	GGGCAAACTGGCTACACTAAACT	55	FP	444	134	GAAAATATTAATTCA
Ya5JW582	AL163151	AATTGCATACACTGGATCACCA	AGAAGCTCTGTCATTGGAAACAG	55	FP	440	123	TGGTTTTCT
Ya5JW583	AL161804	NOT AMPLIFIABLE	NOT AMPLIFIABLE	-	NA	-	-	CCTGACTTAA
Ya5JW584	AL161666	NOT AMPLIFIABLE	NOT AMPLIFIABLE	-	NA	-	-	AAGAAACCTTGGTTGA
Ya5AC2349	CNS01RG1	TGATCGTGTCAAAGCATCTCT	ACGTCTGGGACCTTTCAAGA	60	FP	500	184	AAAGTTGTACTCTAG
Ya5AC2350	CNS05TCV	ACAGACATTGTGGCTAGGGG	ATGCCCAACCTTTACCCTCT	60	FP	1071	757	AAAACAGGTACTGAG
Ya5AC2351a	NG001019	CTCAGGAACCACCAGGAGAG	AGTGCCACCTCATGTCCTGT	60	FP	441	121	AGAATCACCAGACGGCG
Ya5AC2351b	CNS01RGW	GAAGAACCACCAAATCTGCC	TTGAAGATTGCTGCAAAACG	60	FP	458	138	AAGAAAGTGTATTTAG
Ya5AC2352	CNS01DTO	CTCCCATTGGAAGACAATGAA	TCATAATTGGTTGCCCATCA	60	FP	457	144	AAAAACCTTTTTAT
Ya5AC2353	CNS01DVC	GCAATCATGCCAAATCTGTG	ACCCTGAGAGGTCAGGGAAT	60	FP	880	566	ATAGT
Ya5AC2354	CNS01DVS	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AAAAGATATAGATTGG
Ya5AC2355	CNS01RGM	ACCATGCCCAGAGGCTAA	ACCTCACAGGGGCACAAAT	60	FP	500	187	AAAATTCATTTTCTT
Ya5AC2356	CNS01DTY	CCCATGGGTGGTAACTGAAC	TGCTCTGCTACTTGGCTCCT	60	FP	495	178	AAGAAAGGGAAATTCTG
Ya5AC2357	CNS018OX	TGGAGTTCAGGAATAAAGCAGA	TGGGGTGTCAAAGTAGCATTT	60	FP	484	163	AAAAAATGCTTGAATA
Ya5AC2358	CNS05TC9	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AAAAAGTGAAATTTA
Ya5AC2359	CNS00M8V	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	GAAAAATTTG
Ya5AC2360	HSHWRS	TAGACGGACACCTCAGGACC	CAGCCCTTCCCTCTTTTCTC	60	IF	453	126	AAGAATGTTCCAGG
Ya5AC2361	AC073464	TCCTTCCAGAATGGTGTTCC	TGTGTGGAAAACAGTGCCAT	60	FP	1149	834	AAGAGTTTGAGACC
Ya5AC2362	CNS01DXJ	GCACCAATATTCTAGGGCCA	GGTGCTTACACTGTCATGCCT	60	FP	1006	733	AAAGATGGAGTCTT
Ya5AC2363	HSJ215J18	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AAGAAATACATTTTGT
Ya5AC2364	CNS01DTT	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AAAAGCTTTGTGAA
Ya5AC2365	CNS01DTM	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	NONE
Ya5AC2366	CNS01DX4	TTTGGTATGGGTACAATTTTTGC	ACCCAGGTCCTCTAGTCGGT	60	IF	1068	802	AAAAATACAAAAAT
Ya5AC2367	BC029918	TTTGTCTCCACTGGCTGTTG	GGTGCCTCTGGGAATGAGTA	60	FP	472	156	GAGAATGAAGTGC
Ya5AC2368	BC041985	GCTGCACAGTTTGTTTGCTC	CATCTTCACCCCTAGGCAGA	60	IF	421	95	AAAAAGTCAACCTGA
Ya5AC2369	CNS00M8V	TAAGGGTGAATGGGAACCAG	CAATCCAATACCACAGGGCT	60	IF	341	90	AGAAAAAGCCCTGTGG

(table cont.)

Ya5AC2370	CNS05TDT	ATTGCTCTAGCCACGCACTT	AAAGAAACTGACGGGGTCCT	60	HF	487	170	AATATTAGGGAAGGTTT
Ya5AC2371	AC068648	CACCCTGCTTTTTCTTGCTC	AGGTGACCCACCCTTTCTCT	60	FP	1114	799	AAAAAAGAACCTA
Ya5AC2372	CNS01DSK	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	GATTGTGTTTCCT
Ya5AC2373	CNS07EFY	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AAGAGCAGGTTGTT
Ya5AC2374	CNS07EGL	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AAAAAACTCCCCC
Ya5AC2375	CNS01DVS	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	TTTATAGTA
Ya5AC2376	CNS01DRT	GCTCTTCATGGGTTCCTTCA	ACAGAGCCTTCCCTCTGTGA	60	IF	1173	858	AAAAAAGGCAAATGCC
Ya5AC2377	CNS01DT0	GAGCCCTTCGCTAAAGGAGT	TTTGGATGAAAAGAGCAGGG	60	FP	458	151	AAAACTGCCCTGCTC
Ya5AC2378	CNS01DX5	TGCATGTGAACAAAAAGGCT	TTTTGGGAGCGAATCTTTTG	60	FP	486	173	AAAAAAAATTAGAA
Ya5AC2379	CNS07EGN	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	NONE
Ya5AC2380	CNS05TF6	GTGATCACGCTGCTTTATGC	GTGATACAACTCACTATCTGGC	60	IF	468	141	AAGAGAAGCCAGATAG
Ya5AC2381	CNS05TDK	ACGAACCAAAACAGTCTGCC	TCTATGCACAGGGTTTTCCC	60	FP	492	173	AAGAATAGGGAT
Ya5AC2382	CNS01DW9	NOT AMPLIFIABLE	NOT AMPLIFIABLE	-	NA	-	-	CAAAAAGATAAAATATCAA
Ya5AC2383	CNS01DX3	NOT AMPLIFIABLE	NOT AMPLIFIABLE	-	NA	-	-	AAAAAATATAT
Ya5AC2384	CNS01DSZ	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AAGAATATTAACCT
Ya5AC2385	NG_001332	CAAGCTTTAGCATTCTTGCTGTC	GCCTGATCTTTGCATTTTCTG	55	FP	597	290	TTGTA
Ya5AC2386	CNS01DWV	tctcatttgtttgggcttgc	gtccgtagcccacagtttca	55	FP	500	190	AGAAGTAAATTTCC
Ya5AC2387	CNS05TEG	AAATGATGACCTGGGGACAA	TTTGTAAACCAAATCCATTACCA	60	FP	488	171	AAGAAAGTTAGATAC
Ya5AC2388	CNS01DRK	TCGGTTTGTTCAAGATGCAA	CCCAGACTGGTGGAGAAGAG	60	IF	1139	833	AAATAATACTTTTAG
Ya5AC2389	CNS01DTE	TCTTTTCCTCAAAACAAATTCC	TGCGTATTAGTGAAATCATGCAA	60	IF	500	168	TAAACCTTAAATTC
Ya5AC2390	CNS05TEJ	CTCAAATGTTTGCAAAACCC	TTCCCCTGATTGAATTTTGG	60	IF	468	172	AAAAAATGTCCCCAA
Ya5AC2391	CNS018P2	TCTTCCATATCCCTTGTCTGG	TGTAGCCAAGCTGCTCTCAA	60	FP	406	83	AAAATACGTAGCATAG
Ya5AC2392	CNS01DSN	GCTCCAAAATATCTAAATTGCCTC	CCGAGAACATGGCAGAAACT	60	FP	500	194	NONE
Ya5AC2393	CNS01DSU	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AAAAAATGACAATA
Ya5AC2394	CNS01DVY	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AAGAGCTGAGATCTT
Ya5AC2395	BC016865	TTCTCTTTTTCCCTTTGCCA	TCCATCACATTTTCCAGCAA	60	FP	479	167	AAAACTTTTGG
Ya5AC2396	CNS01RIB	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AAAAAGAGTCCAG
Ya5AC2397	CNS01DSS	NOT AMPLIFIABLE	NOT AMPLIFIABLE	-	NA	-	-	GAAAGAAAGAA
Ya5AC2398	AC005533	GCTGGGGTTGGAGTAGACAA	GGGCTCTGACTTGATTGAGG	60	FP	474	157	AAAAGTTCCTTCAG
Ya5AC2399	AC005484	GAGATAATAACCTGAAGGGATTTCA	TTATGGTGGAGTGTGGTGGA	60	FP	409	102	AAAGAAAAATC
Ya5AC2400	AC005520	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	NONE
Ya5AC2401	AC005280	CAAAAGGACTCCCTTGTAGCA	CTACCCACCCATACACCACC	60	FP	1056	728	AATAAGACACCTGATAG
Ya5AC2402	AC005520	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AAAGATAAGTTCAATCG
Ya5AC2403	AC008372	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AATTAGGTGC

(table cont.)

Ya5AC2404	AC078814	GTCAAGGTTCTGGCAGGAAA	TATTCACTCCCTTTCCCCCT	60	IF	491	179	AAGAATTG
Ya5AC2405	CNS07ED1	TACCCCCTGCAATGCTTAGT	CAAACGAACACAAAAATGGAGA	60	FP	496	180	ATTCTCCA
Ya5AC2406	AC007262	NOT AMPLIFIABLE	NOT AMPLIFIABLE	-	NA	-	-	NONE
Ya5AC2407	CNS07EFO	TGCTTGGGAAGGCATAAATC	ATAAGGCCCCTGAGAGCATC	60	FP	1176	856	AGAAAACATACT
Ya5AC2408	CNS01RGP	TGCGCTTTAACACCAGTCAG	AATTATTTGGGGATGGGCTC	60	LF	352	127	AAAGAGAGTGGAAGACC
Ya5AC2409	CNS01RG0	CTGGATCTTGGTTTCCCCTT	GGTTTAGGATTTGCATTGCTG	60	LF	499	172	AAAATCGT
Ya5AC2410	CNS05TDZ	TCTGGCTCCAGAATCCATCT	ATTCACACCCCAAACCAATC	60	IF	472	151	AAAAAACTAATGGTC
Ya5AC2411	CNS01DUM	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AATTACTATAGAG
Ya5AC2412	CNS01DSB	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	NONE
Ya5AC2413	CNS05TBU	GCCAAACATCTATAAAGCATGGAC	TTGGTTAACCCTCATACTTACCC	60	FP	679	373	AAAGAAATCACAATGGA
Ya5AC2414	CNS01DWD	AGAGCCCAAGCTACGTTGAA	TGTTGTGTTGGGAGAGCTTG	60	FP	484	169	AGAAATAAGTATATTTC
Ya5AC2415	CNS05TDR	TTGAGCTGTCACTGTTTGGG	GATGAGGCAATAGCAAACCC	60	FP	476	186	AAGATAAATT
Ya5AC2416	CNS0000R	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AAGAATTGATGAGTG
Ya5AC2417	CNS01DT7	AGAGGCCGTCGGTAAATTCT	TTTTCCCCCTTGGAAAGTCT	60	FP	475	167	AAGATTGCTCTGG
Ya5AC2419	CNS01RGS	AAGGCAGGATGGAAAGAAAAA	CTTCCCAACAATGCAGGAAT	60	FP	1136	835	AAAAATAATGTC
Ya5AC2420	AL160171	TGCACATGTGTCTCCAACAA	GCCCGTACAAAGACAGAAGC	60	FP	430	116	AAGAAACCCTG
Ya5AC2421	CNS00M8S	GGGTCAACCTGCATCTTGTT	GGCACAGAAGCAATCCACTT	60	FP	500	239	AGAATGTTTA
Ya5AC2422	CNS01DS1	ATGTGTGTGATGGAGGCAAA	GCTAAGGGATGGTGTGGAAA	60	FP	1031	692	AGAAATACACA
Ya5AC2423	CNS01DW6	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AAAAAAAACCCA
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Ya5AC2425	AC126335	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AAATAGTAATCCTC
Ya5AC2426	LOC92606	ATGAACCACAGAGAAGCCCA	AACAGAATGCACCCTCTTTAGAA	60	FP	481	175	AAAAAAAATGAAGA
Ya5AC2428	AC117832	CGCTGAATACATCAGGAGCA	TAAAATCAGCAACCTTGGGC	60	FP	1089	775	AAAAATGAAAGACCTG
Ya5AC2429	AC023968	TCTCATCCTTCTTCACTCCTAACA	TGACAATGAAATCCAGCCAA	60	FP	496	195	TAATAATTT
Ya5AC2430	AC110291	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AAAAACTTTA
Ya5AC2431	AC020658	ATACACCGCTCCACTCCATC	ATTTGGAGAAACAGGCCACA	60	FP	442	121	AAGTGTTGTGGCCTG
Ya5AC2432	AC087721	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AAAAAAAAAAATACA
Ya5AC2433	AC066612	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AAGAGTGACCTTTAC
Ya5AC2434	AC084773	GTGCCCCTAGGATGAAAACA	TCTGTAGGCTGAAAAACATTGC	60	IF	457	105	AATAAATTTTTC
Ya5AC2435	AC104041	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	TAAGCTT
Ya5AC2436	AC073964	NOT AMPLIFIABLE	NOT AMPLIFIABLE	-	NA	-	-	AAGAATTAATTTTCT
Ya5AC2437	AC025166	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	NONE
Ya5AC2438	AC039056	NOT AMPLIFIABLE	NOT AMPLIFIABLE	-	NA	-	-	AACATAGGGCTC

(table cont.)

Ya5AC2439	AC117832	TGTGACAAAGTTTGCATTTTGA	AAATTCAGCAAAGTCCATGG	60	FP	492	161	TAGCA
Ya5AC2440	AC090527	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AAAAAAAAAAAATTAG
Ya5AC2441	AC018924	NOT AMPLIFIABLE	NOT AMPLIFIABLE	-	NA	-	-	AAAGAATGGATCTT
Ya5AC2442	AC087433	NOT AMPLIFIABLE	NOT AMPLIFIABLE	-	NA	-	-	AAAAATTT
Ya5AC2443	AC068716	TGAAAATTAGGCCCCCTAAAA	CTCCATCATAGTTGGAAACAGAA	60	FP	452	130	AAATAAGC
Ya5AC2444	AC026523	AAGGAGAAAGGTCAACATGGAA	TGGCTTATCCAGCAATAATGG	60	FP	465	155	AAAAAAATTATG
Ya5AC2445	AC026951	CCATGTTGTCTTGATGCCTG	TGCCCTCCTGCAGTTTTAGT	60	FP	479	164	AAAAAATATTTTAGAGTG
Ya5AC2446	AC124306	CATCTCTTCCCCTCAATCCA	GTGACACTGGGCTTGACAAA	60	FP	416	132	AAAAGCCAGGTT
Ya5AC2447	AC024270	NOT AMPLIFIABLE	NOT AMPLIFIABLE	-	NA	-	-	GAAACTG
Ya5AC2448	AC009562	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	NONE
Ya5AC2449	AC091915	ACCAGAAAAGTAGCCTCGCA	GCTGACCATGCCTACCATTT	60	FP	472	156	AAGAGTGGTTATAG
Ya5AC2450	AC021439	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AAAATTACTCC
Ya5AC2451	AC069382	NOT AMPLIFIABLE	NOT AMPLIFIABLE	-	NA	-	-	ATAATAATTTATTTTC
Ya5AC2452	AC087721	GTTTCAAATGAGGCTGCCAT	TAGACATTTCACCTGGGCCT	60	FP	421	122	AAGAAAATGAATGA
Ya5AC2453	AC016397	NOT AMPLIFIABLE	NOT AMPLIFIABLE	-	NA	-	-	NONE
Ya5AC2454	AC021231	CATCCCTGGAATAAGGCTCA	CGCATTAGAGCTGCTTTTCC	60	FP	466	149	AAAAGACAAAAACCT
Ya5AC2455	AC044787	CTGGGGCCAACCTACTGATA	CAATTGCCAGTCAGCGAGTA	60	FP	395	80	AAAAATGTATAGGCGTG
Ya5AC2456	AC084783	TGTTTTTCCTTGCCACACTG	ACAGCCAGTCTCTTCGTGGT	60	IF	459	142	AAGAGAGAGTAAG
Ya5AC2457	AC012378	NOT AMPLIFIABLE	NOT AMPLIFIABLE	-	NA	-	-	AAAAAAGAGAG
Ya5AC2458	AC013394	TCCCCAACCTTCCTACACTG	GGTAGCCTAAAGGCATGCAA	60	IF	445	132	AAGATTCCAGG
Ya5AC2459	AC079328	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AAAAATTATTTAAGACC
Ya5AC2460	AC068213	TGAGTGAATAAAGGGGTGCAA	ACCTTCTTTGAAACCCCCAC	60	FP	451	149	AAAAAGAGAATGAA
Ya5AC2461	AC104590	TAGATGGGGAGCATGGAAAG	TCTCCAGCCATATGTGACCA	60	FP	429	111	AAGATTTAGAGGGGTG
Ya5AC2462	AC073167	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	NONE
Ya5AC2463	AC105014	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AGAAAAGTGGTTTTC
Ya5AC2465	AC087639	TGATGGAGTTTAAAAAGTGTCAGC	AGCTGCCCTAAGTCACCAGA	60	LF	463	145	AAAAAGTGTCAGCT
Ya5AC2466	AC091230	GTGCTTAAGGACAGGGGTCA	AGCGAGGGAGTGAATGAATG	60	FP	464	146	AAAAAGAGGCTATTG
Ya5AC2467	AC026636	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AAAAAAGCTG
Ya5AC2468	AC015726	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	TTTGAG
Ya5AC2469	AC027559	AGAAGTCGCAAGATGCCTGT	GCTTTCAGCCAGTTCCTGAC	60	FP	850	544	AAACAGTGAATGT
Ya5AC2470	AC110607	NOT AMPLIFIABLE	NOT AMPLIFIABLE	-	NA	-	-	NONE
Ya5AC2471	AC091100	AACAAAGTGCTGTTGCTGGTT	AGCATTATTGTCACCCCGAG	60	FP	1100	761	AAATAG
Ya5AC2472	AC090751	TCAGAAGAGGAAATGGCAGG	CCAATTGCAGCATGAGAAGA	60	FP	1170	890	AAAATTATTACAC
Ya5AC2473	AC025919	TTGCTCCCACAGCTTAGACC	TCCAAGTTTGCGCTTCTTTT	60	FP	1090	771	AAAGAAGGGCATTACA

(table cont.)

Ya5AC2474	AC010674	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AAATAAATAGA
Ya5AC2475	AC135626	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AAGAAATATTTG
CHROMOSOME 16								
Ya5NBC52	AC009094	NOT AMPLIFIABLE	NOT AMPLIFIABLE	-	NA	-	-	GAAAACTTTTCTTCC
Ya5NBC57	AC009107	GACGTAAAGAGATGTTGTTAAGTGAAAAT	ACTGTAGGAGGTAAATGGAAAGTC	60	IF	444	126	AGAAATTCATATATGCA
Ya5NBC81	HU95742	NOT AMPLIFIABLE	NOT AMPLIFIABLE	-	NA	-	-	GGTGATGGATTG
Ya5NBC173	AC003977	NOT AMPLIFIABLE	NOT AMPLIFIABLE	-	NA	-	-	AAAAGTTTATTTTTCAG
Ya5NBC309	AC020663	CCTCTACCTGCTGGGTTCAA	CCCAGGGACTCTCCAGAAA	55	FP	425	114	TGCCCGGCTA
Ya5NBC336	AC007151	AGGCCCACATCACTGTAAGG	TGATCCATAGCTCTTTTTGTGC	60	FP	486	172	AAAGACTTTC
Ya5 411	AC007011	CAGCCGGTTCTTTAGGAGAG	AGCCTGTGCCTACGACACTT	55	FP	418	95	CCCATTCCCTGATTTTT
Ya5 452	AC004493	CCAAGCTTGACGCTTTTGTA	CAGGCACTTGAGGAAGTGTG	57	FP	447	130	GGGAGTATTTTT
Ya5 453[2]	U91321	ATGAAAAGGGCCCTGAAATC	TTGCAGATGCCTAGGGAAATA	55	IF	401	80	TTCAGTGTCTATTCTT
Ya5 464	AC002289	TTGGTCAATATCGCTCATGG	TGGGAGTTAGGAAAAACTTGG	57	HF	400	67	AAAGCTGTAGG
Ya5 473	U67230	CCTGTTTGGAGAATGGAGGA	GCCATTGCATGTCTCCAGTA	58	FP	394	86	GAATCACTT
Ya5 531	AF265340	GCAAACACAGTGCCACAAGT	TGGGGATGTGACCCAAGTAT	60	IF	502	195	TGTTGTGTA
Ya5 536	AC009079	TCCACTGCCAACATTTGTCT	GAGAAAAGGACTCAGAACGTCA	60	FP	444	81	CANNOT FIND WORD FILE
Ya5AC2476	AC079412	TTTCCAGGAGAAGGGAAAGC	TTGCTGGATTTTTCCTTTGA	60	FP	493	172	AAAATACATTGTATAACTCAG
Ya5AC2477	AC092120	TGGAATTTGTAGTCTTTTGAGTCTG	GTCAGAGTGGTGGGGTGTTC	60	FP	391	85	AAGACTC
Ya5AC2478	AC079412	TGCTCCCTTCTCTCTGGAAA	GACCTCATTTGGAGAATGCC	60	FP	430	101	AATATTCCTACTACAGATTTTT
Ya5AC2479	AC092123	CCTCGTGGAGTAACGGTGTT	CTTCAGACCTCCTCACCTCG	60	FP	1089	776	AACAGG
Ya5AC2480	AC027275	AACCACACCAACCAAATGTGT	GCATGTGAATTGACTGCTGAA	60	IF	421	131	AAAAGTGAATTCAG
Ya5AC2481	AC130650	TGGAAAAATGCAAATGGACA	TGCATACTGACATATTTGGGC	60	FP	465	153	AAGAATCAT
Ya5AC2482	AC092325	TTCCTGGCTGGAATTCAAAA	TTGCAATGTGCTAGAATGTTAAA	60	FP	500	177	AAAAATATACTCTG
Ya5AC2483	AC008741	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AAAAATACAGACATTAG
Ya5AC2484	AC027688	NOT AMPLIFIABLE	NOT AMPLIFIABLE	-	NA	-	-	AAGAGTGTTTTTAGCC
Ya5AC2485	AC009061	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AAAAAGACATCTTAAAAAGA
Ya5AC2486	AC133548	NOT AMPLIFIABLE	NOT AMPLIFIABLE	-	NA	-	-	AAAAGACAGGCCC
Ya5AC2487	AC140873	TTTCAAATGCCTAGTGCAATTACT	TGCACACACGCTCACTGATA	60	LF	490	179	AAAATCAATTGGTA
Ya5AC2488	AC134305	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AAGACAAATGCAG
Ya5AC2489	AC009090	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AAAGAAAATGTG
Ya5AC2490	AC016647	CATTGGCAGTGGGTGTGTAG	GGAGTCTCTGAAGGATGGCA	60	FP	464	136	AAGATTTATCTG
Ya5AC2492	AC026470	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AGAAAATAGTAAATTAAG
Ya5AC2493	AC023813	CTCCCCTCTCTCCTACCCAG	CTACCTTGCCTTTCCCACTG	60	FP	494	172	AATAATATTTCACCTG

(table cont.)

Ya5AC2494	AC023827	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AAAACTCAACAATA
Ya5AC2495	AC007603	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AAAAGCACAGATTT
Ya5AC2496	AC044798	CCTGATTGTGTGTAAAAGGGG	ACTGCCTGTTCAGCAAACCT	60	FP	495	177	AAAAGGGGACACATACTA
Ya5AC2497	HUAC002400	TGGGTGTTGGAAGGCTATTC	CAGGAGCAGATGGAAGGAAG	60	FP	1198	885	AGAAAAAAATTAGCTGGG
Ya5AC2498	AC109600	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AAAAGTGTGTGGC
Ya5AC2499	AC123908	TTGGGTTCAGAAACACCCAT	GGTGTCTGAATTTACCCCTTCA	60	FP	500	236	AGATCAAAATTTG
Ya5AC2500	AC009154	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AAGAATCTC
Ya5AC2502	AC130464	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AAGAAAATAGCTCTTTGT
Ya5AC2503	HUAC003003	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AGAACTGAGCCTAGG
Ya5AC2504	AC018552	TGGAGCCTGAGATTCACACA	CACCTGCACAACCGTCTATG	60	FP	500	191	AAAAAGAGGAAACTGA
Ya5AC2505	AC008870	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AAAGCTGGG
Ya5AC2506	AC018553	GGGAAAGGGCTTTTTGTTGT	GAGCAGGGGGTCTGTCTTTA	60	FP	477	165	AAGATTGACAAAGATTG
Ya5AC2507	AL354855	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AATATGGTGAAACCCCG
Ya5AC2508	AC009111	TGGCAAGCTGGAAATCTACC	AAGCCTGGGTCAAATCCCTA	60	FP	500	182	AAGAATAAGTCATTC
Ya5AC2509	AC106793	CCTCCTATGAGCTCAGTCCCT	TCAAAAACACCTCCTAAAGTCTACC	60	FP	497	184	AAAAGGAATATGC
Ya5AC2510	AC092126	TTTCCCAGAGGATCGTGAAC	TCAAGTTAAATTCATGCATCGG	60	FP	475	152	AGAAATTATCCGATGC
Ya5AC2511	AC009081	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AAAAATGTGTATTATC
Ya5AC2512	AC009147	CAGCTGTAGTATGCTGGGCA	ATGGAGCTGACCATCTTGGA	60	FP	482	165	GAAAAATGCCTGAATCTTG
Ya5AC2513	AC093520	CAGCTGCTTCCCAAAGAAAC	CATTGAAGGGAATTCATGGG	60	FP	412	92	AAAGAAACCATGCCCC
Ya5AC2514	AC010289	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	NONE
Ya5AC2515	AC018846	ATTAGCTTTCGTTTGACGCC	TGGAACCACATCAGGCATAA	60	FP	498	190	AAAGCAATGGGTTA
Ya5AC2516	AC044802	CTCTCTCAACTACCAGCCGC	AAAACCCTCAAATTCCTGCC	60	FP	453	129	AAAGACTTTAGGGCAGGA
Ya5AC2517	AC007225	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	NONE
Ya5AC2518	AC109599	CTGAGCATGTCAGTGGCCTA	GCAGTCCACGTTTGCAGTTA	60	FP	462	127	AACAGTATTAC
Ya5AC2519	AC009061	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AAAAAGACATCTTAAAAGA
Ya5AC2520	AC026474	TGAAAATGTTTCTGAGGCCTTTA	CTTGGAGCTCATTGGTCCTT	60	FP	496	191	NONE
Ya5AC2521	AC099314	NOT AMPLIFIABLE	NOT AMPLIFIABLE	-	NA	-	-	AAAAATTAGCCGGGTGTG
Ya5AC2522	HUAC003964	GATGAGAGGCCATTTCCCTT	AAAGAGGCTGCTCAATTTGC	60	FP	470	159	AAAAGAAAAACCTTAG
Ya5AC2523	AC010547	TTTCATGGCACAGGGTGTTA	CTTCTCAGGGCTGTTTGGAG	60	FP	452	140	AAAAGAGCTCTTGCCA
Ya5AC2524	AC092289	CATCCCTGACTCCGATCCT	GTTTAATCCCCTGGGCAAAT	60	FP	489	188	AAAGATTCTGA
Ya5AC2525	AC010748	CTGAGAGCTCCACGAGGGTA	TCCATGGAAGAAGCAACACA	60	IF	499	194	ATCTAT
Ya5AC2526	AC009127	AGCCAAGTGGAAGTGTTGCT	TGAGAAGTGTGTGTGTGTCCA	60	FP	498	188	AAAGATGGACACACAC
Ya5AC2527a	AC046158	AAACGTGAAAAGCAATTTACAAAA	TCCTATCCAGAGACAAGCACTG	60	FP	456	132	AGACACGTAC
Ya5AC2527b	AC106729	TTCTCCAACACCCCTCAATC	TGGGAACAGAAAAAGGTTGG	60	FP	1100	780	AAAAAGAAAGTACC

(table cont.)

Ya5AC2528	AC007223	NOT AMPLIFIABLE	NOT AMPLIFIABLE	-	NA	-	-	AATAGAAGATACGG
Ya5AC2529	AC140890	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AAAACACCTTTGGC
CHROMOSOME 17								
Ya5NBC102	AF118569	TCCCATTTCTCTAGACCTGCTG	CCCATAACAGGTCTTCATATTTCC	55	IF	483	194	ATACAGTCACTTTT
Ya5NBC120	AC005863	GGACCACATGACTGAGTGTAAAGT	GAGGTGGCCTCTTAACCATAATTC	55	IF	518	199	AGAAATGACATTAAGAG
Ya5NBC122	AC005747	CCATTCATTCTATTTGGGGAGTTAG	GACTAAACCAGGATGTGAGCTTTT	53	FP	527	217	AAAAGTGTTCT
Ya5NBC126	AC005144	GTCTGCTGAATGATTAAACCAACAC	GTGCCATTTCTACTACTGAAACCTA	60	FP	480	171	GCTTCACTTCT
Ya5NBC157	AC005281	CATACGTTAAATCACTCGGTACTCA	TCAGAAAAGTATACAGGTGATGTGC	60	HF	516	207	AAAAGCAAACCCA
Ya5NBC160	AC005245	CTCAGCTGTGCCTGATACTCTATAA	GCCTACTGGATAAGTCACACATTTT	55	IF	551	234	AAACATACTTTTGGG
Ya5NBC162	AC003957	ATGAGCAAGTCTACATATTCCTCCA	CTTGTTGCTGTCAAGGGTCTAATA	60	FP	481	167	AAAGACAGATGA
Ya5 421	AC005988	GAGGCTGTGACTGCAAAGTG	TTCGGTGTTCCAAAAACAGAC	60	IF	493	177	AAGAAATGACATCTG
Ya5 423	AC005553	ACCTCATGACCAGCAGGAAC	CCCCAAACCATGTTGTTTTT	58	FP	485	152	AGGGATG
Ya5 431	AC005962	AACGCACACATTTCCAACCT	TGGCACAGATTGCCTACTCA	60	FP	432	121	GGAAATAAT
Ya5 433	AC005900	TGACTCCCTTTTGGAAATCCT	GGCTTTGTCCAAGCATTGAG	60	FP	462	120	GCCTGCTTCCTGTTT
Ya5 435	AC005495	CTGGCGACTAAGGTGAAAGC	AAAAGGTAATCCCTCTATCCTCTTG	60	IF	407	96	CCAAATAGACTTCTT
Ya5 444	AC005323	ATCATTGCTGCTGCACAAAA	GAGCACCCTTTCAACGCTAT	60	FP	534	222	CAGTTTTTC
Ya5 450	AC003962	CTGTCATCTTACAGAAGCCTTGAA	CCAGCAGGATACTGGTTTGA	60	FP	508	192	AAAAAGAAATGAATT
Ya5 454	AC003664	AAGCCTAGGACACACGCATAA	TGCTTGGCACTTAGTGTTAGGA	59	IF	418	91	GGTAAAGACAGAATCTTT
Ya5 514	AC022596	NOT AMPLIFIABLE	NOT AMPLIFIABLE	-	NA	-	-	AAGATTTAACTCT
Ya5AC2530	AC105105	TGGATGTCTGAATTGATGGG	CCCCTGGTTCCAAAGTTTTT	60	FP	1170	842	AATTAT
Ya5AC2531	AC105105	TGGATGTCTGAATTGATGGG	CCCCTGGTTCCAAAGTTTTT	60	FP	403	99	AAAAAAAAAAATCA
Ya5AC2532	AC023389	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AAGAGTAATTGGGGG
Ya5AC2533	AC132938	CTCATCCCACAGCTGGATCT	CTTTAGGATCGGCACCTCTG	60	FP	497	190	AAGAAGTGAAATGTG
Ya5AC2534	AC005291	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AAAAACTAG
Ya5AC2535	AC006435	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	NONE
Ya5AC2536	AC092713	ATGAGGCCGGACAATGTAAG	AAGGGTGGGAGTTTTCCTTG	60	FP	488	173	AAGATTTAGATGAAGC
Ya5AC2537	AC127512	GAAAATCCAATACATTAATTCACCA	AAGAGGACGTGGAGCAAAAA	60	FP	465	154	AAAAATTAATTTATG
Ya5AC2538	AC015842	NOT AMPLIFIABLE	NOT AMPLIFIABLE	-	NA	-	-	AAAGAAATCTGCCCG
Ya5AC2539	AC124283	AGTTGACAGGTTTTGCCACC	CAAGACAGGTAACGCAGCAA	60	IF	1018	713	AAAAATGAGTCCTG
Ya5AC2540	AC104024	NOT AMPLIFIABLE	NOT AMPLIFIABLE	-	NA	-	-	AAGAATAGTACAATAA
Ya5AC2541	AC005284	GCCATCTCATGAAGACCCTC	ATTTTCCTCTTCCGTTTGGC	60	FP	431	108	AAGAAGTGAGCAGCCA
Ya5AC2542	AC012146	ACCACTGGTCCTCAGTTTGG	TCAGTACGTTGTGAATGAGGC	60	FP	463	150	AAAAAGCCTCATTCA
Ya5AC2543	AC007982	CTCACTGAGCGTTACCATGC	TTTCACAATACTTGTAGGGCAAGA	60	FP	486	174	AAGAGGTAGTAGG

(table cont.)

Ya5AC2544	AC068442	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AACAAGGAGATT
Ya5AC2545	AC068025	ACACACAAATGGTTGCCAGA	CTCCCATTTCAGTTCCCCTT	60	FP	752	438	AAACAGTAAAAAGAA
Ya5AC2546	AC011840	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AAGAGTTCTTTGT
Ya5AC2547	AC027821	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AAGAGCTACATCTGG
Ya5AC2548	AC024614	GCAGCTGCACAGATTACCAA	TAAGTCACTGTTCTGGCCCC	60	FP	1147	829	AAAAGCCATATGAG
Ya5AC2549	AC015938	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AAAGAAGTACACTT
Ya5AC2551	AC068669	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AAAGAGGTATAAAAA
Ya5AC2552	AC103703	TGAAGGGAAACTGAGTTGCAT	AAATGCCCCAACCCTACTCT	60	FP	457	137	AAAAAATTTGATATC
Ya5AC2553	AC027801	NOT AMPLIFIABLE	NOT AMPLIFIABLE	-	NA	-	-	AAGAATCTGATGTG
Ya5AC2554	AC091133	CAGGGAAGGTGGTTGCTCTA	TGGCACAACCTGTGTGTCTT	60	FP	484	162	AAGAATTTCCTGCTC
Ya5AC2555	AC069454	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	NONE
Ya5AC2556	AC015876	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	NONE
Ya5AC2557	AC087496	ACATGCAATATAAAAATAGCCAACT	TGCATTGCGCGTTAACTAGA	60	FP	469	164	AAAAATAGCCAACTAAA
Ya5AC2558	AC087596	NOT AMPLIFIABLE	NOT AMPLIFIABLE	-	NA	-	-	AAGACCTG
Ya5AC2559	AC025521	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AAAAAATTTGTTTTGG
Ya5AC2560	AC005962	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AAAAAGATATGC
Ya5AC2561	AC099850	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	GCCTGTA
Ya5AC2562	AC007114	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	NONE
Ya5AC2563	AC011073	GAACCCAGGTGGTAGACACG	GACCAAGACCAGAAGACCCA	60	FP	484	181	AAGAAAATAATA
Ya5AC2564	AC068025	NOT AMPLIFIABLE	NOT AMPLIFIABLE	-	NA	-	-	NONE
Ya5AC2565	AC099850	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AAACATTGACCAC
Ya5AC2566	AC025048	AGCAAGACGAAAAGGCAAAA	CCTGAATGCTGCATGTGATT	60	FP	457	144	AAGAGAACAAGTC
Ya5AC2567	AC025858	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AAGTTGAATTGGG
Ya5AC2568	AC018628	AAACAGTCAACTTCCGGTGG	AAGCAATGTAACATGAAGTGGAGA	60	FP	462	151	AAGAATAAGTGAGTCAC
Ya5AC2569	AC090615	TATCTCCTTGCATTCCCCTG	TCAATTCCTTTCATCTGGGC	60	FP	805	486	AAAAAGATTTGGGA
Ya5AC2570	AC005495	NOT AMPLIFIABLE	NOT AMPLIFIABLE	-	NA	-	-	AAAAATGATTCAGTTC
Ya5AC2571	AC005242	CCACAAATTCTTAAAGCCCA	GCCACAAGCTACGAGGAAAA	60	IF	462	136	AAGAGTATCATTA
Ya5AC2572	AC006448	GATAAGCCAATGAAGCCAGC	ATTTTTGTCCTGCCGTTGAC	60	FP	456	135	AAAAACAAGATACA
Ya5AC2574	AC087301	NOT AMPLIFIABLE	NOT AMPLIFIABLE	-	NA	-	-	NONE
Ya5AC2575	AC104981	CCCACCAGTTGCTCAAGATT	TGCTGGCTTCTCCTTCCTTA	60	FP	384	69	AAGATTTAGAGCA
Ya5AC2576	AC055863	GTGCAGCTAACCAAGGCTTC	TCGGATTGTGTGTGGTAGGA	60	FP	461	142	AAGGATTCCAT
Ya5AC2577	AC018665	GCTTTTTCAGCATGTTTGCTT	AACCACACACTCACTCACGC	60	IF	465	148	AAAAATAGAACTCCC
Ya5AC2578	AC116025	GGGCACTTATCAAGCACCTC	CTGGAGGATGTGGCTCTTTC	60	FP	425	116	ACCTCTCT
Ya5AC2579	AC142472	NOT AMPLIFIABLE	NOT AMPLIFIABLE	-	NA	-	-	NONE

(table cont.)

CHROMOSOME 18

Ya5 432	AC005968	CCCCAAACCAATCAAGTAGG	GGCTTTTCCACTTCATGACAA	60	HF	425	83	GACCATTAGTTTTTT
Ya5 530	AC010854	CACTTTCACTCCCTCCCAAG	TGCAGCTATTGCCTCCTTTT	60	FP	425	108	GTCTT
Ya5AC2580	AC091137	NOT AMPLIFIABLE	NOT AMPLIFIABLE	-	NA	-	-	GAATG
Ya5AC2581	AC120349	TATCACTTTGGCAGGGAAGC	TGCTTAAGTTTTCCTATTTTGCC	60	FP	450	172	AAAAAATTAGCATAGT
Ya5AC2582	AC121320	NOT AMPLIFIABLE	NOT AMPLIFIABLE	-	NA	-	-	NONE
Ya5AC2583	AC034110	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AAAGATCAGAG
Ya5AC2584	AC091067	TTCCAGAGATGACATGGACA	AAAAAGAAGCCTGGAGAGGG	60	IF	496	180	AAAGAGTCAATTAGT
Ya5AC2585	AC107878	TCTTGCAACCTACATACGCC	TGTGCTCACTCTCCTGACCA	60	LF	488	161	AAAAGTGAGA
Ya5AC2586	AP001032	TCCTTCCTTGTTATTTGCGTTT	ACTGGCCTCCCTATAAAATGA	60	FP	497	186	AATAGAATGACTT
Ya5AC2587	AP005212	GTAAGCCTGGCAGAAGGAAT	GACAAGGCAATTTGGTCTGA	60	FP	500	183	AAAAAGAGCA
Ya5AC2588	AC105245	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AAAAAACATGGTA
Ya5AC2589	AC034110	TGTTCATCAAAAAGAGGTTGGA	GCACGAGCATAAAATTCCAG	60	FP	373	63	AAAAAGAGGTTGGATA
Ya5AC2590	AC023932	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AAAAGAAAAGGCATT
Ya5AC2591	AC068473	AGTGGGCAGGGTTCACATAG	CCCTGGCACTCAACAAACTT	60	FP	500	187	AAAGAATGGCTTATT
Ya5AC2592	AC103949	GGGAGGATTATGTTGAAGCAA	GATGGCAGGTAGAATCAAAGC	60	FP	491	187	AAAAGAAAAATAC
Ya5AC2593	AP005139	AAGTGACCGTGAAATCCTGC	TTTATGACGTCTGTTGGGGG	60	FP	469	173	AAATCACATTCTC
Ya5AC2594	AC090812	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AAGAATAGTTCA
Ya5AC2595	AC103768	CCATCACTCTGCCCACTCTT	CAGGAAAGGCATTTTCCTAGC	60	FP	476	169	AAGAGTAGCTAG
Ya5AC2596	AC026839	TGCAAGTAACAAATGCCCAA	ACAAGCACTGCCCTCTGATT	60	LF	463	140	AAAGAAATCAGAGGG
Ya5AC2597	AC007998	GCACCCCCAGTAGTCACAGT	CAGTTATCCTCATGGTGGCA	60	FP	461	141	AAAATGCCACCATG
Ya5AC2598	AC103768	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	CAGCATT
Ya5AC2599	AC091495	ACTGATGGGGTGTGGAGAAG	GTCAGGAGCTCTGGTTCTGG	60	FP	1000	682	AAAAATCACAGTAGG
Ya5AC2600	AC034299	GGCAAATATGGTTGTCAATTTTC	CCTTGTCTTTTACACCAGGCA	60	FP	478	164	AAAAAATTAGTTAT
Ya5AC2601	AC055820	TCTCCTCCTACCTCGTCTTTTT	CCAGAAGGTAAAACTCTGGTTCA	60	FP	499	153	ATAAAACACACTTTA
Ya5AC2602	AP005228	AATTCACTCCCATTGTCCCA	TGAGGACAGCATTTCTGTGAA	60	FP	439	126	AAAAATGTGATAAGGT
Ya5AC2603	AC021311	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AAAGACTAAAATCTA
Ya5AC2604	AC105074	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	NONE
Ya5AC2605	AC021538	TGCAAGCGGTTATTGAAACA	TCATTACTTCCCCACGGACT	60	FP	1123	795	AAAAAATGATGGATCG
Ya5AC2606	AC105074	ATGCTTTCAACTCCCCCTTT	GGGGTGGAATCTCAGCTCTA	60	FP	438	119	AAGATAGGCACTACTG
Ya5AC2607	AP005229	TGGTTAAGAAAGCAAGGCCC	TTCCATTTTTAAATTTTCTCCCTG	60	FP	396	87	AAGAAAGCAAGG
Ya5AC2608	AC048380	TCGTCTCTACCTCCAAGGAAA	TTTTGGCTGAAGTCCACAGA	60	LF	459	142	AGAAAATAGGTATCATGG
Ya5AC2609	AC121320	CGACCTCTGCTCCCAATATC	CTGTAATGACAGAAGTTCCGTTT	60	FP	1168	831	ATGACAGTGCT
Ya5AC2610	AC008021	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	NONE

(table cont.)

Ya5AC2611	AC027458	CATTGTTGCATTGCACCTTC	AAATTTGTTTCCAGTATGGGC	60	FP	477	176	TTGAAA
Ya5AC2612	AC093462	NOT AMPLIFIABLE	NOT AMPLIFIABLE	-	R	-	-	NONE
Ya5AC2613	AP001269	TGGGGTTGGCATTTTTCTTA	CTCTGCTGCAGCGTGTCTA	60	IF	496	182	GAAAAAGAAATAA
Ya5AC2614	AC009717	TTCTGAGTAGGTGTGCCCAA	GAATGCATTGTCTTCAAAGCTAAG	60	FP	394	107	AGAACTTAGCTTTG
Ya5AC2615	AC093462	TCAGATGAAGTTTGATTTCTGAAG	AGCACTGGAAATGTTTGAGACT	60	FP	473	160	AAAAAATAGAAAGTTG
Ya5AC2616	AC016382	GCAATGGAATAAGTCACAATAGGA	CCATTTGCATCTTTTCTCCTC	60	FP	426	105	AACAAAGAGGAGA
Ya5AC2617	AC090324	TGACAAGCACAGGACTGACC	ATTGGCTGATTCCAAAGCAC	60	LF	390	84	AATAATAATGTTTG
Ya5AC2618	AC022031	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AAAAGAACAAAGCCAG
Ya5AC2619	AC018994	CCGCCACTGTACAGATAAGAAA	AGTTAGGCACATGGACTGGG	60	FP	423	115	AGCAACC
Ya5AC2620	AC016229	TTTGTGCATGCTTGAGAACA	CAGATATTGCTGATGCTGCC	60	FP	479	166	AGAAGAAACTAGGTT
CHROMOSOME 19								
Ya5NBC150	AF135028	AAATGGAGACACAGAGGTGTAAAGA	CCCAAACTGCATATTTAAAGGGTAG	60	IF	491	169	CTATGATCATCTTCTTT
Ya5NBC191	AC007191	TGACGGGTGAGATGTATATAGAAGC	ACTCTTCTCATCTGTGTCAATTTGG	60	FP	645	330	AATCTTG
Ya5NBC202	AC004603	ACGCTCCAAAGTCCTCACCT	TGGAAGCTGGTTCTTCAGTG	60	FP	487	154	AGAAATACAGGAGG
Ya5NBC230	AC000100	NOT AMPLIFIABLE	NOT AMPLIFIABLE	-	NA	-	-	AAAGTATTCTTCTTCT
Ya5NBC349	AC011504	TCAAGAACTGTGGGCCAAAT	GGATGTTGTCACAGCAGCAT	60	HF	469	53	CCTGAACCTGTTCTT
Ya5 416	AC006539	TGCATTCATCCAGCACTGTT	GCATAAGGCCCAGTCAAGAG	60	IF	463	153	TCAATCTATTCCT
Ya5 428	AC006131	GAACCCTGGCAGAAATGCTA	GGGCCTTCTTGGATTTCACT	60	FP	467	169	ACACTAAGTC
Ya5 439[2]	AC005784	CATATCTGCACGGTGTGACC	CATGGCTTAGTGGTTTTCCA	60	FP	425	110	GATACTTTTCTTTT
Ya5 446[2]	AC005257	ACCCATCCACAACGTTTCTT	TGGGTTACTGTATGGGTGGA	60	FP	405	120	GGGAGTATTTTT
Ya5 447	AC005261	AGACCCAGTGGTTGCTATGC	CAAAGGGACGACAAAATTGC	60	FP	489	180	ATCTCAGGGATATTT
Ya5 512	AC016627	TCATTCACAGGGGAGTACTGTG	CCCTCCTGTAACAAATGCTG	58	FP	429	119	AAGAGGACACTCC
Ya5 523	AC078899	TTGGCTGAAAAGAGACTTCACA	CCTCTGCATTTGCCTCCTT	55	FP	399	83	CAACTTAGAACTTTTT
Ya5AC2644	AC011495	NOT AMPLIFIABLE	NOT AMPLIFIABLE	-	NA	-	-	AAAAAATTAG
Ya5AC2645	AC016629	TTTGGCAGTCTGAAGGGAAC	CCTTCCTCCTTCCTTTCCTG	60	FP	410	93	AAAAAGAAAATAGTG
Ya5AC2646	AC006131	GAACCCTGGCAGAAATGCTA	GGGCCTTCTTGGATTTCACT	60	FP	467	169	ACACTAAGTC
Ya5AC2647	AC123912	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	NONE
Ya5AC2648	AC026803	GGTTTCAGCTAATAGGCCCC	CTTGGCAAGAACAGACCCAT	60	FP	1135	831	AAAAAAACTGTCTT
Ya5AC2649	AC022432	ACATCAGGAGGGTGAACGAC	ATAGACAACCACGGCCTGAC	60	FP	865	355	GAGCAGAGGGCA
Ya5AC2650	AC011455	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AAAGAAAACCTGAG
Ya5AC2651	AC005785	NOT AMPLIFIABLE	NOT AMPLIFIABLE	-	NA	-	-	AAGAGAATGGCATGAA
Ya5AC2652	AC073541	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AAAAAAAGTATTTCC
Ya5AC2653	AC092296	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AAAAATCTTACCTT

(table cont.)

Ya5AC2654	AC008739	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	GAAAATTAAAAATCT
Ya5AC2655	AC027319	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	NONE
Ya5AC2656	AC027319	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AGGAAG
Ya5AC2657	AC016586	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	GAAAATGGGAGCGTGC
Ya5AC2659	AC138473	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AAAACAAAGATGG
Ya5AC2660	AC010508	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AAGAAAAAGAAATTTTCC
Ya5AC2661	AC010615	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	NONE
Ya5AC2662	AC010467	CCAAGGGCCAAGTCTATCAA	CACTTGAATTTCATACCAGCCA	60	IF	435	120	AAGAGTGAGGCAA
Ya5AC2663	AC018758	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AAAAGTGGCAATTTCC
Ya5AC2664	AC011531	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	TGTGTTAAATGTT
Ya5AC2665	AC011462	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	GAAAAAAAT
Ya5AC2666	AC008751	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	NONE
Ya5AC2667	AC008403	AATGCAAACCAGTCAGAGGG	GGCTTCTAGGTCACTCAGCG	60	FP	783	455	AGGAAGAATGTTCCA
Ya5AC2668	AC008751	NOT AMPLIFIABLE	NOT AMPLIFIABLE	-	NA	-	-	AAGAGGCTGGG
Ya5AC2669	AC022409	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AAAGAACTAGA
Ya5AC2670	AC128673	TGGGCAGAGTGAATATCCTTTAG	GACCTTGGTCCTTATTGTCTTCC	60	IF	476	159	GAAAATGGCTTTCAC
Ya5AC2671	AC011481	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	NONE
Ya5AC2672	AC011484	NOT AMPLIFIABLE	NOT AMPLIFIABLE	-	NA	-	-	NONE
Ya5AC2673	AC008687	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	NONE
Ya5AC2674	AC008733	CATTGCCATCAGAACACCAC	TTGTTCTTCTCGAAAAACTCCA	60	FP	377	58	AAAAGAAATACTA
Ya5AC2675	AC008752	NOT AMPLIFIABLE	NOT AMPLIFIABLE	-	NA	-	-	AAAAGTATTACCAG
Ya5AC2676	AC011467	NOT AMPLIFIABLE	NOT AMPLIFIABLE	-	NA	-	-	AGAAGGGCCAGTCATG
Ya5AC2677	AC008532	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	NONE
Ya5AC2678	AC007193	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	NONE
Ya5AC2679	AC007204	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AAGAGATTGTAG
Ya5AC2680	AC011477	TCAATGTAACTACAATGCTTCAAAA	AAGGCACTGACACTTCAGACA	60	FP	446	116	AAATCTACTACTTTTA
Ya5AC2681	AC012313	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	NONE
Ya5AC2682	AC008686	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AATAATAATAATAG
Ya5AC2683	AC008746	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	GAAAGAAAGG
Ya5AC2684	AC006271	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AGAAATACCATTCT
Ya5AC2686	AC008507	TGGGTCAGGCATCTGTTGTA	ACGGATGTATTTCTGGCTGG	60	FP	1085	775	AGAAAGGGGAAAGTTGAG
Ya5AC2687	AC002128	ACTTCAGCCATCCCAATCAC	AAAGTCTGGAGCTGGGGTTT	60	FP	489	191	AAGAACAAGG
Ya5AC2688	AC092080	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AAAAGTGGTTTAATTG
Ya5AC2689	AC008744	NOT AMPLIFIABLE	NOT AMPLIFIABLE	-	NA	-	-	AAAACGCTTTCGGG

(table cont.)

Ya5AC2690	AC008474	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AAAGAAATAGGG
Ya5AC2691	AC005621	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AAAAAATACAAAAACT
Ya5AC2692	AC007773	ACAGAACCGAAAATTGGACG	GATGTGGTAGTGCGAGCTGA	60	FP	475	163	ATACTGCCTC
Ya5AC2693	AC008751	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AAAGAAAAAAAGACATCTG
CHROMOSOME 20								
Ya5NBC10	AC008725	AAAGCATAAAGAAAAGTACGCCAAC	CAATGAAGATATAGAACAGCCCCTA	60	FP	449	141	AAAAGCGTTTGGG
Ya5NBC45	AL049868	TAGGGTAAGGAATATGTGCTGCTTTAG	GTCTCTGAACGACTATGTGAGCAG	60	IF	591	265	GAAAATCTTTTATA
Ya5NBC87	AL109830	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	GAAAATACAGGATA
Ya5NBC100	AL035683	NOT AMPLIFIABLE	NOT AMPLIFIABLE	-	NA	-	-	CAATGTTGTG
Ya5NBC139	AL031650	TGAAAGCTCTTAAGGTCTTCTCTCT	TAAGTAGACCAGAAACAGGGAACAG	60	FP	851	634	CCTAAATTTC
Ya5NBC141	AL096769	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AATAATAATGTGCA
Ya5NBC145	AL035667	TGCATCCTCTTCTGCTGTTC	AATTGGGTTCACTAGACAAAGG	60	FP	500	276	NONE
Ya5NBC148	AL031659	ACAAGATGACAGATGTAAACCCAAC	AAGGTGTTGTCAGACTAATCTATCG	60	IF	505	193	AAATGATTGATCTT
Ya5NBC180	AL109618	CTTGAAGATCGCCATGAGTAGA	GGCATTTCTTTGGACTTGTCTC	55	FP	525	211	TGTTTAGATTTTT
Ya5NBC302	AL035665	CCTGCATACCCACACATACC	GGCAGTCAGCTTTTGACCTC	65	FP	395	72	TTCACTCTCTTTT
Ya5NBC329	AL121892	TTTTTCCCCTGTAGTTGGACA	TTGTTCAGGAGAGGGAAGGA	60	FP	465	154	TTAGTGATGACTCTT
Ya5NBC331	AL121593	TTCATGGCGAAAGCTTGATA	AGCTCCTGGCCAGATTAACA	62	FP	414	92	TGAAATAATCAGTATT
Ya5NBC353	AL034549	CCATGTAACCTGGTAGACCTTT	GTTCAGCGGGAACAGTGAGT	60	FP	432	119	AAAACTGTTTGG
Ya5 438	AL031257	GCAGGCAAAGGGTGAGTTAC	CCTGGGCTCTGAAGAAGTTG	60	FP	424	97	AAAGGAACAGGCCA
Ya5 542	AL121897	TTTGGATTTCCAACAGCTCA	GGGGGTACGTGGGTGTTACT	55	LF	477	185	AGAACA
Ya5 548	AL389883	GCATTCCAAAAGTATACATGCAA	AATTATTGCAGAGAGCACAGGAA	60	FP	439	159	TGTTTCTT
Ya5 550	AL359954	GCAGACATTTGCAGAGAATCC	CACCAGGGTTCCACAAAGAT	60	LF	451	119	GAGTGG
Ya5 551	AL117382	TGGCATAAGAAACTGCTGTCA	GCTCCAGAACTCCAGATCCA	55	FP	405	104	TGTCTTAAAT
Ya5 556[2]	AL359695	AGACTCAGCTGCTCCTCCAG	TTGTTTTGGCTTAAATTCTTTCC	55	FP	461	145	NONE
Ya5 558[2]	AL136143	CAACCTTGAAACGTTGATTAATTT	CCAAGGCATAGAGCCACTTC	60	FP	459	130	AAACTTTTTT
Ya5 563[2]	AL354745	AACAAGGGGAAATCTGGACA	CAGGCCTCTTCCCTAGCTTC	55	LF	424	75	AGAATGCCATGTGA
Ya5 564[2]	AL049868	TTCTGGGGTTTGGATTGTGT	AGCTGGGTCTCTGAACGACT	60	IF	443	116	GAAAATCTTTTATA
Ya5 565[2]	AL354773	GGTTCCTAGCCCTGGACACT	GGCTTTCTTAATACCAGTCAAGC	60	FP	454	136	TATAAACTTTA
Ya5 567[2]	AL121582	TTCAATCATTTTCACCTTTTGC	GTGAATTGCCAGCATTCTAATC	60	IF	412	100	AAATACATTATC
Ya5JW575	AL050349	CACTGTTATTAGCAATGCCCACT	GGGGGAAGAGGTTTGAATCTTA	60	FP	508	194	TTATTAAATATTTTA
Ya5AC2694	AL135940	NOT AMPLIFIABLE	NOT AMPLIFIABLE	-	NA	-	-	AAAGAAGTG
Ya5AC2695	AF314058	AAGGACTCCATCCCAGGTCT	ATCTAAGAGGCAGCTGTGGC	60	FP	386	70	AAGAACTGTGCTC
Ya5AC2696	HS1013A22	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	NONE

(table cont.)

Ya5AC2697	AC005914	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AAAAAAAAAAGGAAGA
Ya5AC2698	HSDJ553F4	GGTGTCATTTCTGCCATCACTAT	CTAGCAAAACTCACAGTCAAGCA	60	HF	447	127	ACAGTCATTTT
Ya5AC2699	HS1080B10	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AAAAATGAAGCAAGC
Ya5AC2700	HSBA379J5	AGACAGCTGCTGGTTCGATT	GGCTCTCTTCGTTCCTGTTG	60	FP	863	544	AAACATGTG
Ya5AC2701	HSJ841K13	TTCTTCTGAACCCCAAAGGA	ACCCTGCCTTTTGAAGGAGA	60	FP	494	177	AAAAATTGTATTA
Ya5AC2702	HS1065O2	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AAAAAAGTTG
Ya5AC2703	AL133339	NOT AMPLIFIABLE	NOT AMPLIFIABLE	-	NA	-	-	AAGAAATGGCCCTCTT
Ya5AC2704	AL136173	GGTTCCTGTCCTCCACTTCA	TCCTCTCCTCCCAAGTCTCA	60	IF	498	165	AAAAACTACCCTACTGGAGT
Ya5AC2705	AL160414	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AAAAATCAGCTGG
Ya5AC2706	HSBA19D2	TCAACTTGGCTTATGTCTGAAAA	TACCAAAAGCATTGGCATCA	60	IF	449	136	AAAAATGTATTGTC
Ya5AC2707	HSDJ901O8	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AAATAAATAAATAG
Ya5AC2708	HSDJ686N3	NOT AMPLIFIABLE	NOT AMPLIFIABLE	-	NA	-	-	AAAAGTCCTTTACTCTC
Ya5AC2709	HS1107C24	CTTTTCCTGGGGCACAATTC	AGGCCTACAGCAGTTGCCTA	60	IF	471	166	AAAAAACCACTCAC
Ya5AC2710	HS64K7	GTAGGCAGACACTGGGTGCT	TACACAGTGGGCACTCAAGC	60	FP	497	199	AGGAAGCTTG
Ya5AC2711	HS616B8	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AGAAATAAGAGCAAGAG
Ya5AC2712	HS28F12	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AAAAAGTGGAAACAA
Ya5AC2713	AL450465	NOT AMPLIFIABLE	NOT AMPLIFIABLE	-	NA	-	-	AGAATTTAACCAGATAATTCTT
Ya5AC2714	HS633O20	AAGACAAACTTTCACGCTGGA	TTTTTATGTCATTTTGTGTTACGTG	60	FP	384	74	ACACAGTTATG
Ya5AC2715	AL136090	TGCTGTCTGAGTGAGATGGG	ATGAACCTTCGAAATGCCTG	60	IF	1180	867	AAAAGAGGCCCTGG
Ya5AC2716	AC093536	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AAAAAATCAATAA
Ya5AC2717	HS859D4	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AAAAGAATAAATTTCTG
Ya5AC2718	HSJ1123D4	GCCACTGAATGGGGTAAAAG	TGTAAGTCTTTGCCCAATAAGAAA	60	FP	473	159	AAGAAATGTACTAC
Ya5AC2719	AL139352	GGAAAAGCCAAAAACAAAAACA	CCCCAAAACAAGATCCAAAA	60	FP	500	182	AAAAAGATTTTCTT
Ya5AC2720	HSDJ777D9	NOT AMPLIFIABLE	NOT AMPLIFIABLE	-	NA	-	-	AACATAGATGA
CHROMOSOME 21								
Ya5NBC24	AJ011932	AAAATTGAGAGACGAGGAGAAGGT	CCTCATCAATACTGTAACTGTCAC	60	LF	595	286	GATCTTTA
Ya5NBC26	AP000311	GGGCTATTCTGATTTTCTTCTTCTC	AGAAGAGACATCACTACAGATACTA	55	FP	476	158	TAATATTCTCTTATTTA
Ya5NBC121	AJ011932	AGGGGGAAAACATCAAAAACTC	CCTCATCAATACTGTAACTGTCACA	60	FP	510	202	GATCTTTA
Ya5NBC164	AF042090	CTGCTGACTTTGAACTTAAACTGC	GATGGAAGATGTCTTAGGGTTCTCT	60	FP	503	190	NONE
Ya5NBC305	AP000966	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	CATTTTTATTT
Ya5NBC315	AP000474	GTAGACACCGCAGGCAACTC	AAAAGGATCCGTAAGAAGGAGA	62	FP	444	134	AAAAAATGTGGAATA
Ya5NBC351	AP000459	TTCCTCCCCTTTTTCCTGTT	TGTCAGTATGTAAACCCATGCT	55	IF	437	123	CAGATAATTTTTTT
Ya5 445	AJ006996	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AGAAACATAGATCTAGGG

(table cont.)

Ya5 448	AF038667	AAGAGTGCACTGTGGTTGAAAA	GGACAGCCTGACTTAATCTCAA	60	LF	592	277	NONE
Ya5AC2721	AP001729	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AAAAGGCCATGCTGT
Ya5AC2722	HS21C013	NOT AMPLIFIABLE	NOT AMPLIFIABLE	-	NA	-	-	AGAAATCTCCCATGATG
Ya5AC2723	AP001253	TTGCAAGAGTATCAAAAGGGG	AGAGCAATTTGGGGACCATT	60	FP	416	167	AAGAACTAC
Ya5AC2724	AP000282	CTGTTGGACGCTCTCAGAAGAT	TGCAGCTGCTCAGATTCCAG	60	FP	433	167	AAGAAGTGGGTG
Ya5AC2725	HS146B4	NOT AMPLIFIABLE	NOT AMPLIFIABLE	-	NA	-	-	AGAAAATACCTAGA
Ya5AC2726	AF131217	NOT AMPLIFIABLE	NOT AMPLIFIABLE	-	NA	-	-	AATAATTAGTTGCT
Ya5AC2727	AP000239	NOT AMPLIFIABLE	NOT AMPLIFIABLE	-	NA	-	-	ATAAATGTGGTG
Ya5AC2728	AP001675	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AAAATTGCAGCTGA
Ya5AC2729	AP001059	NOT AMPLIFIABLE	NOT AMPLIFIABLE	-	NA	-	-	AAATAAAAAACA
Ya5AC2730	AP000161	NOT AMPLIFIABLE	NOT AMPLIFIABLE	-	NA	-	-	AAAAACAGCCCAGGTG
Ya5AC2731	AP001346	ACCTCACTCAGAACTCAACGAAG	ATGATACCCTTTTCTCAGCACAC	60	IF	429	103	AAGAAGCATTTC
CHROMOSOME 22								
Ya5NBC2	M28713	CTTTAGACTACAGTTGTGTTAGCCTCTTG	CTGCACTTTCCAAATTTTCTACCAC	55	FP	710	384	AGCATTT
Ya5NBC13	AL031302	CTTCCTGTGTATACTTCTCTGCAC	GTCTGTGACCTGCAACACAAG	60	FP	604	291	NONE
Ya5NBC31	AL033543	GTATCTTGTGTGTTTCCTAACAAGACTGAG	CTCATTTTCACTTATCAGGTCT	60	FP	523	238	AGAAAGTTCATAGG
Ya5NBC42	AL078621	AGTAAGTCCCTCCCCATATGCT	GGTCTTTCTAACCCAAAGGTCAC	55	FP	486	185	AGAC
Ya5NBC109	AC005745	GTGCCTGGTACTCTAGAAATAAAACTCTCT	AGAATGAAACTCCGGCTCAAA	58	IF	561	251	TCTTGTATGACTCTTT
Ya5NBC129	AL008635	TACATGGAGTTAGAGCCCGTTC	ACAAGTGGCTGTCACYCAACAC	60	FP	486	180	AAAAGAGCGGACCCT
Ya5NBC146	AL022329	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	NONE
Ya5NBC221	AC004019	CAGTTTTCCATATACATGTGGGTTC	TAGTGTTAAGAGGCCCATTTTCTAC	60	IF	640	313	CTGGACCCTGTTCT
Ya5NBC223	AC005006	GTTCTCTGTAAAATGGACCAATCAG	CATAGACCTTCCCAGTGAGTGTTAC	60	LF	455	214	GCAGTTGAAGTTTT
Ya5NBC224	BK407F11	ACATGCTTTCCCATTATGTGTG	CCAAGTGGCAGTAATAGACTCTGTC	55	FP	502	195	NONE
Ya5NBC225	AC002470	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	NONE
Ya5NBC226	DJ323M22	CCTCCACGGACTCCTAATTACA	GTGGCCCTGAGAAGGAATTT	55	FP	421	130	NONE
Ya5NBC228	AC004832	ACTGCATGCCAGCCTCA	GCTAGTTACAATGAAAATGTGCTGT	55	FP	842	529	TGTGATAAATATG
Ya5NBC229	AL096873	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	NONE
Ya5NBC231	BA422A16	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AAAATTAGCCAGGTTT
Ya5NBC314	AC016025	GTTCCAGGGGGAAATGAAAT	GTGGGGCACTGTGTGATTC	60	FP	392	70	AAAAGGAAACTCAGGA
Ya5AC2732	HS633O19	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AATCCCAGCACTTTGG
Ya5AC2733	AP002414	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	AAGAAAAGGTAATTTTT
Ya5AC2734	HS109G6	NOT AMPLIFIABLE	NOT AMPLIFIABLE	-	R	-	-	AAAAAAATCATAG
Ya5AC2735	HS243E7	INSERTED IN REPEATS	INSERTED IN REPEATS	-	R	-	-	NONE

(table cont.)

1. Amplification of each locus required 2:30 min @ 94^{o} C initial denaturing and 32 cycles for 1 min @ 94^{o} C, 1 min Annealing Temperature (A.T.) and 1 min elongation at 72^{o} C. A final extension time of 10 min at 72^{o} C was also used.
2. Elements at the end of sequencing contigs are denoted (EC), those residing in other human repeats are denoted (R) and those elements with inconclusive PCR results (NA). Elements represented here are classified according to allele frequency as: high frequency (HF), intermediate frequency (IF), low frequency (LF) or as fixed present (FP) insertions. Fixed Present: every individual tested had the Alu element in both chromosomes. Low frequency insertion polymorphism: the element is present in no more than 1/3 (33%) of alleles tested. Intermediate frequency insertion polymorphism: the element in present in more than 1/3 (33%) of alleles tested and no more than 2/3 (67%) of the alleles. High frequency insertion polymorphism: the element is present in no more than 2/3 (67%) of all alleles tested.
3. PCR Product Sizes: Empty product size is calculated computationally by removing the Alu elements and 1 direct repeat from identified filled site. In cases where target site duplication sequence were not found flanking the element PCR product sizes may vary from those reported.

Table 4 – Ya-lineage autosomal associated human genomic diversity.

	African American					Asian/Alaskan Native[4]					European					South American					
	Genotypes					Genotypes					Genotypes					Genotypes					
Elements	+/+	+/-	-/-	f[1]	Het[2]	+/+	+/-	-/-	f[1]	Het[2]	+/+	+/-	-/-	f[1]	Het[2]	+/+	+/-	-/-	f[1]	Het[2]	Avg Het[3]
CHROMOSOME 1																					
YA5ACA589	13	5	1	0.82	0.31	6	1	4	0.59	0.51	13	1	2	0.84	0.27	8	4	3	0.67	0.46	0.39
YA5ACA593	6	8	4	0.56	0.51	15	3	2	0.83	0.30	18	0	0	1.00	0.00	18	0	0	1.00	0.00	0.20
YA5ACA636	19	1	0	0.98	0.05	12	7	0	0.82	0.31	3	16	0	0.58	0.50	19	0	0	1.00	0.00	0.21
YA5ACA637	11	5	4	0.68	0.45	7	7	3	0.62	0.49	14	4	0	0.89	0.20	11	8	1	0.75	0.38	0.38
YA5ACA641	0	1	19	0.03	0.05	1	10	7	0.33	0.46	1	8	7	0.31	0.44	1	2	14	0.12	0.21	0.29
YA5ACA630	5	13	1	0.61	0.49	0	1	17	0.03	0.06	1	7	10	0.25	0.39	1	5	13	0.18	0.31	0.31
YA5ACA614	1	7	12	0.23	0.36	0	4	14	0.11	0.20	1	5	12	0.19	0.32	0	3	14	0.09	0.17	0.26
YA5ACA645	7	8	4	0.58	0.50	11	5	3	0.71	0.42	18	1	0	0.97	0.05	13	3	1	0.85	0.26	0.31
YA5ACA654	0	1	19	0.03	0.05	0	0	14	0.00	0.00	0	0	13	0.00	0.00	0	0	8	0.00	0.00	0.01
YA5ACA659	0	2	17	0.05	0.10	0	2	18	0.05	0.10	0	1	16	0.03	0.06	0	1	18	0.03	0.05	0.08
YA5ACA647	0	13	3	0.41	0.50	18	0	0	1.00	0.00	14	2	2	0.83	0.29	12	0	0	1.00	1.04	0.46
YA5ACA662	20	0	0	1.00	0.00	15	5	0	0.88	0.22	20	0	0	1.00	0.00	18	2	0	0.95	0.10	0.08
YA5ACA618	18	2	0	0.95	0.10	14	3	0	0.91	0.17	18	0	0	1.00	0.00	9	2	2	0.77	0.37	0.16
YA5ACA733	11	9	0	0.78	0.36	1	4	14	0.16	0.27	12	4	4	0.70	0.43	8	9	3	0.63	0.48	0.39
YA5ACA728	0	2	14	0.06	0.12	0	0	14	0.00	0.00	0	0	14	0.00	0.00	0	0	12	0.00	0.00	0.03
YA5ACA720	3	4	7	0.36	0.48	6	6	1	0.69	0.44	7	2	2	0.73	0.42	7	5	1	0.73	0.41	0.44
YA5ACA745	3	13	2	0.53	0.51	8	7	3	0.64	0.47	6	7	0	0.73	0.41	6	3	3	0.63	0.49	0.47
YA5ACA975	4	7	7	0.42	0.50	15	4	1	0.85	0.26	6	9	2	0.62	0.49	9	5	2	0.72	0.42	0.42
YA5ACA974	11	7	1	0.76	0.37	6	9	5	0.53	0.51	13	5	4	0.70	0.43	3	7	6	0.41	0.50	0.45
YA5ACA769	1	6	12	0.21	0.34	0	3	17	0.08	0.14	1	9	10	0.28	0.41	0	4	16	0.10	0.18	0.27
YA5ACA759	0	3	15	0.08	0.16	1	4	14	0.16	0.27	4	9	6	0.45	0.51	2	5	10	0.26	0.40	0.33
YA5ACA702	0	3	17	0.08	0.14	0	0	20	0.00	0.00	0	0	20	0.00	0.00	0	0	20	0.00	0.00	0.04
YA5ACA707	0	10	4	0.36	0.48	0	0	15	0.00	0.00	0	9	5	0.32	0.45	0	0	8	0.00	0.00	0.23
Ya5NBC347	17	2	1	0.90	0.18	4	7	8	0.39	0.49	7	8	2	0.65	0.47	10	2	4	0.69	0.44	0.40
CHROMOSOME 2																					
YA5ACA784	0	0	20	0.00	0.00	0	0	20	0.00	0.00	0	0	20	0.00	0.00	0	0	20	0.00	0.00	0.00
YA5ACA792	20	0	0	1.00	0.00	20	0	0	1.00	0.00	18	2	0	0.95	0.10	20	0	0	1.00	0.00	0.02
YA5ACA796	3	12	5	0.45	0.51	5	10	5	0.50	0.51	5	12	3	0.55	0.51	9	7	3	0.66	0.46	0.50
YA5ACA791	2	5	10	0.26	0.40	7	4	5	0.56	0.51	1	2	16	0.11	0.19	1	0	17	0.06	0.11	0.30
YA5ACA807	15	3	2	0.83	0.30	20	0	0	1.00	0.00	20	0	0	1.00	0.00	19	1	0	0.98	0.05	0.09
YA5ACA815	2	14	2	0.50	0.51	3	15	2	0.53	0.51	2	16	0	0.56	0.51	4	14	0	0.61	0.49	0.51
YA5ACA828	5	3	11	0.34	0.46	1	0	17	0.06	0.11	0	0	14	0.00	0.00	0	0	13	0.00	0.00	0.14
YA5ACA825	3	11	5	0.45	0.51	3	10	6	0.42	0.50	8	7	3	0.64	0.47	2	8	8	0.33	0.46	0.49
YA5ACA862	11	5	3	0.71	0.42	1	3	15	0.13	0.23	4	4	12	0.30	0.43	6	3	8	0.44	0.51	0.40
YA5ACA804	17	3	0	0.93	0.14	20	0	0	1.00	0.00	20	0	0	1.00	0.00	20	0	0	1.00	0.00	0.04
YA5ACA868	18	2	0	0.95	0.10	20	0	0	1.00	0.00	10	9	1	0.73	0.41	17	3	0	0.93	0.14	0.16
YA5ACA866	0	1	19	0.03	0.05	1	9	10	0.28	0.41	12	4	4	0.70	0.43	10	5	2	0.74	0.40	0.32
YA5ACA877	1	5	14	0.18	0.30	0	5	17	0.11	0.21	3	11	4	0.47	0.51	1	10	6	0.35	0.47	0.37
YA5ACA864	0	0	20	0.00	0.00	0	0	17	0.00	0.00	0	0	16	0.00	0.00	0	0	17	0.00	0.00	0.00
YA5ACA891	0	5	15	0.13	0.22	1	13	6	0.38	0.48	0	13	7	0.33	0.45	1	9	10	0.28	0.41	0.39
YA5ACA928	5	10	5	0.50	0.51	0	1	19	0.03	0.05	5	7	8	0.43	0.50	7	7	6	0.53	0.51	0.39
YA5ACA914	0	0	20	0.00	0.00	0	0	20	0.00	0.00	0	0	20	0.00	0.00	0	0	20	0.00	0.00	0.00
YA5ACA924	7	11	0	0.69	0.44	13	6	0	0.84	0.27	8	10	1	0.68	0.44	7	11	1	0.66	0.46	0.40

(table cont.)

YA5ACA917	1	7	12	0.23	0.36	9	9	2	0.68	0.45	10	8	2	0.70	0.43	12	7	1	0.78	0.36	0.40
YA5ACA921	0	5	15	0.13	0.22	0	0	20	0.00	0.00	0	0	20	0.00	0.00	0	0	20	0.00	0.00	0.06
YA5ACA949	11	9	0	0.78	0.36	17	3	0	0.93	0.14	20	0	0	1.00	0.00	20	0	0	1.00	0.00	0.13
YA5ACA953	3	10	3	0.50	0.52	7	1	3	0.68	0.45	11	2	1	0.86	0.25	10	3	0	0.88	0.21	0.36
YA5ACA937	1	8	10	0.26	0.40	0	0	18	0.00	0.00	0	0	17	0.00	0.00	0	0	17	0.00	0.00	0.10
YA5ACA912	0	17	3	0.43	0.50	0	10	8	0.28	0.41	0	4	16	0.10	0.18	0	7	12	0.18	0.31	0.35
YA5ACA903	8	9	2	0.66	0.46	4	6	9	0.37	0.48	6	12	2	0.60	0.49	11	5	3	0.71	0.42	0.46
YA5ACA814	6	13	1	0.63	0.48	15	5	0	0.88	0.22	10	8	1	0.74	0.40	18	2	0	0.95	0.10	0.30
Ya5NBC5	2	5	5	0.38	0.49	3	2	8	0.31	0.44	1	6	11	0.22	0.36	2	8	4	0.43	0.51	0.45
Ya5NBC324	0	8	1	0.44	0.52	0	15	2	0.44	0.51	0	14	4	0.39	0.49	0	15	1	0.47	0.51	0.51
Ya5JW499	0	2	13	0.07	0.13	0	0	19	0.00	0.00	0	0	18	0.00	0.00	0	1	16	0.03	0.06	0.05
CHROMOSOME 3																					
YA5ACA1063	2	15	3	0.48	0.51	1	9	9	0.29	0.42	4	3	9	0.34	0.47	2	6	12	0.25	0.38	0.45
YA5ACA1048	3	6	8	0.35	0.47	3	12	2	0.53	0.51	9	8	0	0.76	0.37	11	5	1	0.79	0.34	0.42
YA5ACA1054	11	3	3	0.74	0.40	20	0	0	1.00	0.00	12	4	4	0.70	0.43	18	2	0	0.95	0.10	0.23
YA5ACA1070	17	3	0	0.93	0.14	20	0	0	1.00	0.00	20	0	0	1.00	0.00	20	0	0	1.00	0.00	0.04
YA5ACA1100	2	14	4	0.45	0.51	16	4	0	0.90	0.18	18	0	0	1.00	0.00	20	0	0	1.00	0.00	0.17
YA5ACA1003	16	2	1	0.89	0.19	13	4	1	0.83	0.29	17	2	0	0.95	0.10	11	2	3	0.75	0.39	0.24
YA5ACA1024	2	14	3	0.47	0.51	6	12	2	0.60	0.49	10	8	2	0.70	0.43	12	4	3	0.74	0.40	0.46
YA5ACA1011	2	6	12	0.25	0.38	0	1	18	0.03	0.05	0	0	20	0.00	0.00	0	0	20	0.00	0.00	0.11
YA5ACA1002	8	7	5	0.58	0.50	0	0	20	0.00	0.00	5	9	7	0.45	0.51	6	4	9	0.42	0.50	0.38
YA5ACA1134	0	5	15	0.13	0.22	0	1	19	0.03	0.05	0	0	20	0.00	0.00	0	0	20	0.00	0.00	0.07
YA5ACA1130	19	1	0	0.98	0.05	20	0	0	1.00	0.00	14	6	0	0.85	0.26	14	2	2	0.83	0.29	0.15
YA5ACA1086	0	3	16	0.08	0.15	0	0	20	0.00	0.00	0	3	17	0.08	0.14	0	5	14	0.13	0.23	0.13
YA5ACA1020	8	9	3	0.63	0.48	7	6	6	0.53	0.51	13	6	1	0.80	0.33	10	6	4	0.65	0.47	0.45
YA5ACA1052	0	0	20	0.00	0.00	0	0	20	0.00	0.00	0	0	20	0.00	0.00	0	0	20	0.00	0.00	0.00
YA5ACA1050	9	10	1	0.70	0.43	10	2	0	0.92	0.16	9	9	2	0.68	0.45	11	5	3	0.71	0.42	0.37
YA5ACA1071	3	8	9	0.35	0.47	8	6	3	0.65	0.47	4	9	4	0.50	0.52	7	4	4	0.60	0.50	0.49
YA5ACA1044	6	9	3	0.58	0.50	13	5	1	0.82	0.31	8	8	4	0.60	0.49	9	6	4	0.63	0.48	0.44
Ya5NBC51	4	10	3	0.53	0.51	5	6	8	0.42	0.50	6	7	7	0.48	0.51	3	8	9	0.35	0.47	0.50
CHROMOSOME 4																					
YA5ACA1145	6	6	7	0.47	0.51	2	7	10	0.29	0.42	7	4	8	0.47	0.51	1	4	12	0.18	0.30	0.44
YA5ACA1158	10	8	1	0.74	0.40	8	9	3	0.63	0.48	4	10	2	0.56	0.51	2	12	3	0.47	0.51	0.48
YA5ACA1161	12	8	0	0.80	0.33	16	3	1	0.88	0.22	10	9	1	0.73	0.41	17	2	1	0.90	0.18	0.29
YA5ACA1174	8	6	6	0.55	0.51	1	3	17	0.12	0.21	3	8	9	0.35	0.47	5	4	11	0.35	0.47	0.41
YA5ACA1185	15	4	1	0.85	0.26	19	1	0	0.98	0.05	19	1	0	0.98	0.05	20	0	0	1.00	0.00	0.09
YA5ACA1184	1	4	14	0.16	0.27	18	2	0	0.95	0.10	9	4	3	0.69	0.44	17	2	0	0.95	0.10	0.23
YA5ACA1168	10	6	2	0.72	0.41	16	2	1	0.89	0.19	12	2	2	0.81	0.31	7	1	0	0.94	0.13	0.26
YA5ACA1153	4	3	11	0.31	0.44	8	5	0	0.81	0.32	1	5	7	0.27	0.41	7	1	1	0.83	0.29	0.37
YA5ACA1233	1	6	13	0.20	0.33	2	8	9	0.32	0.44	0	1	16	0.03	0.06	0	2	17	0.05	0.10	0.23
YA5ACA1250	6	9	3	0.58	0.50	17	0	1	0.94	0.11	13	6	0	0.84	0.27	20	0	0	1.00	0.00	0.22
YA5ACA1251	12	7	0	0.82	0.31	20	0	0	1.00	0.00	8	11	1	0.68	0.45	9	9	1	0.71	0.42	0.30
YA5ACA1242	10	2	4	0.69	0.44	1	3	11	0.17	0.29	0	0	11	0.00	0.00	1	0	14	0.07	0.13	0.21
YA5ACA1259	16	4	0	0.90	0.18	20	0	0	1.00	0.00	19	1	0	0.98	0.05	19	1	0	0.98	0.05	0.07
YA5ACA1257	6	8	6	0.50	0.51	3	8	7	0.39	0.49	2	14	4	0.45	0.51	2	8	9	0.32	0.44	0.49
YA5ACA1202	0	0	20	0.00	0.00	0	0	20	0.00	0.00	0	1	19	0.03	0.05	0	2	18	0.05	0.10	0.04
YA5ACA1197	0	0	20	0.00	0.00	0	0	20	0.00	0.00	0	1	19	0.03	0.05	0	0	20	0.00	0.00	0.01
YA5ACA1204	9	4	6	0.58	0.50	13	3	3	0.76	0.37	18	2	0	0.95	0.10	14	5	0	0.87	0.23	0.30
YA5ACA1274	10	7	3	0.68	0.45	20	0	0	1.00	0.00	19	1	0	0.98	0.05	20	0	0	1.00	0.00	0.13

(table cont.)

YA5ACA1172	2	2	13	0.18	0.30	0	1	15	0.03	0.06	0	2	13	0.07	0.13	0	0	17	0.00	0.00	0.12
Ya5NBC61	10	6	3	0.68	0.44	5	2	10	0.35	0.47	9	7	1	0.74	0.40	8	4	5	0.59	0.50	0.45
CHROMOSOME 5																					
YA5ACA1292	0	2	18	0.05	0.10	4	9	6	0.45	0.51	0	3	17	0.08	0.14	1	8	11	0.25	0.38	0.28
YA5ACA1360	1	6	12	0.21	0.34	2	8	9	0.32	0.44	0	1	20	0.02	0.05	0	2	18	0.05	0.10	0.23
YA5ACA1355	4	9	7	0.43	0.50	3	9	5	0.44	0.51	2	7	11	0.28	0.41	2	8	7	0.35	0.47	0.47
YA5ACA1370	19	0	1	0.95	0.10	16	3	0	0.92	0.15	16	3	1	0.88	0.22	20	0	0	1.00	0.00	0.12
YA5ACA1376	9	7	4	0.63	0.48	11	5	2	0.75	0.39	17	3	0	0.93	0.14	20	0	0	1.00	0.00	0.25
YA5ACA1320	1	10	9	0.30	0.43	6	12	1	0.63	0.48	11	8	0	0.79	0.34	11	8	1	0.75	0.38	0.41
YA5ACA1318	6	12	2	0.60	0.49	12	7	0	0.82	0.31	15	5	0	0.88	0.22	5	3	2	0.65	0.48	0.38
YA5ACA1352	2	9	7	0.36	0.47	2	10	7	0.37	0.48	2	13	4	0.45	0.51	5	7	5	0.50	0.52	0.49
YA5ACA1410	2	9	9	0.33	0.45	4	8	7	0.42	0.50	4	7	9	0.38	0.48	2	5	12	0.24	0.37	0.45
YA5ACA1339	0	2	16	0.06	0.11	1	10	8	0.32	0.44	0	4	16	0.10	0.18	1	8	11	0.25	0.38	0.28
YA5ACA1400	7	4	8	0.47	0.51	10	1	1	0.88	0.23	11	3	0	0.89	0.20	13	2	2	0.82	0.30	0.31
YA5ACA1436	2	13	6	0.40	0.49	0	6	14	0.15	0.26	5	8	6	0.47	0.51	5	5	9	0.39	0.49	0.44
YA5ACA1368	3	5	12	0.28	0.41	10	7	2	0.71	0.42	6	6	7	0.47	0.51	8	5	4	0.62	0.49	0.46
Ya5NBC123	5	7	7	0.45	0.51	6	5	4	0.57	0.51	14	5	1	0.83	0.30	11	5	1	0.79	0.34	0.41
Ya5NBC311	13	2	2	0.82	0.30	11	4	2	0.76	0.37	15	3	1	0.87	0.23	11	5	1	0.79	0.34	0.31
Ya5NBC16	20	0	0	1.00	0.00	20	0	0	1.00	0.00	10	10	0	0.75	0.38	20	0	0	1.00	0.00	0.10
Ya5NBC18	17	1	0	0.97	0.06	18	1	0	0.97	0.05	20	0	0	1.00	0.00	20	0	0	1.00	0.00	0.03
Ya5JW513	0	0	20	0.00	0.00	0	0	20	0.00	0.00	0	0	20	0.00	0.00	0	0	20	0.00	0.00	0.00
CHROMOSOME 6																					
YA5ACA1441	2	11	3	0.47	0.51	14	4	0	0.89	0.20	14	6	0	0.85	0.26	15	4	0	0.89	0.19	0.29
YA5ACA1504	4	11	2	0.56	0.51	8	9	2	0.66	0.46	9	10	1	0.70	0.43	12	7	0	0.82	0.31	0.43
YA5ACA1516	0	0	20	0.00	0.00	0	0	20	0.00	0.00	0	0	20	0.00	0.00	0	0	20	0.00	0.00	0.00
YA5ACA1583	12	3	1	0.84	0.27	20	0	0	1.00	0.00	20	0	0	1.00	0.00	20	0	0	1.00	0.00	0.07
YA5ACA1579	9	3	5	0.62	0.49	9	5	6	0.58	0.50	5	9	6	0.48	0.51	4	9	7	0.43	0.50	0.50
YA5ACA1458	1	4	14	0.16	0.27	0	4	16	0.10	0.18	0	0	19	0.00	0.00	0	0	20	0.00	0.00	0.11
YA5ACA1467	7	5	7	0.50	0.51	14	0	0	1.00	0.00	5	5	1	0.68	0.45	3	3	3	0.50	0.53	0.37
YA5ACA1480	18	2	0	0.95	0.10	20	0	0	1.00	0.00	18	2	0	0.95	0.10	18	2	0	0.95	0.10	0.07
YA5ACA1549	13	4	1	0.83	0.29	7	8	3	0.61	0.49	13	7	0	0.83	0.30	10	4	3	0.71	0.43	0.37
YA5ACA1572	5	8	5	0.50	0.51	1	5	14	0.18	0.30	4	10	6	0.45	0.51	2	8	9	0.32	0.44	0.44
YA5ACA1574	3	5	11	0.29	0.42	1	6	12	0.21	0.34	4	7	7	0.42	0.50	3	9	6	0.42	0.50	0.44
YA5ACA1555	4	6	5	0.47	0.51	17	0	0	1.00	0.00	4	10	2	0.56	0.51	14	1	1	0.91	0.18	0.30
YA5ACA1561	5	12	0	0.65	0.47	14	5	0	0.87	0.23	12	6	0	0.83	0.29	18	2	0	0.95	0.10	0.27
YA5ACA1571	0	8	9	0.24	0.37	0	2	17	0.05	0.10	1	5	13	0.18	0.31	1	6	13	0.20	0.33	0.28
YA5ACA1570	1	9	8	0.31	0.44	3	10	7	0.40	0.49	2	2	16	0.15	0.26	1	3	15	0.13	0.23	0.36
YA5ACA1497	2	7	9	0.31	0.44	0	2	16	0.06	0.11	2	7	8	0.32	0.45	4	7	8	0.39	0.49	0.37
YA5ACA1491	0	4	13	0.12	0.21	0	9	9	0.25	0.39	0	3	14	0.09	0.17	1	3	12	0.16	0.27	0.26
YA5ACA1492	3	9	7	0.39	0.49	3	12	5	0.45	0.51	5	10	5	0.50	0.51	5	10	5	0.50	0.51	0.51
YA5ACA1532	0	2	18	0.05	0.10	0	0	20	0.00	0.00	0	6	12	0.17	0.29	0	0	18	0.00	0.00	0.10
YA5ACA1508	1	1	15	0.09	0.17	0	0	10	0.00	0.00	0	2	11	0.08	0.15	2	0	8	0.20	0.34	0.16
Ya5NBC132	3	2	3	0.50	0.53	9	0	0	1.00	0.00	13	0	0	1.00	0.00	11	0	1	0.92	0.16	0.17
Ya5NBC327	2	9	9	0.33	0.45	13	6	1	0.80	0.33	19	0	0	1.00	0.00	7	6	1	0.71	0.42	0.30
Ya5NBC171	0	0	20	0.00	0.00	0	0	20	0.00	0.00	0	0	19	0.00	0.00	0	0	20	0.00	0.00	0.00
Ya5NBC54	0	0	14	0.00	0.00	0	2	12	0.07	0.14	0	1	8	0.06	0.11	0	1	7	0.06	0.13	0.09
Ya5NBC197	0	0	20	0.00	0.00	0	0	20	0.00	0.00	0	0	20	0.00	0.00	0	0	19	0.00	0.00	0.00
Ya5JW434	4	3	1	0.69	0.46	14	3	0	0.91	0.17	15	3	0	0.92	0.16	10	0	0	1.00	0.00	0.20
Ya5JW557	0	6	9	0.20	0.33	0	0	20	0.00	0.00	0	4	16	0.10	0.18	0	2	18	0.05	0.10	0.15

(table cont.)

CHROMOSOME 7

YA5ACA1598	4	7	8	0.39	0.49	10	8	2	0.70	0.43	13	4	3	0.75	0.38	7	8	3	0.61	0.49	0.45
YA5ACA1727	7	7	3	0.62	0.49	10	9	1	0.73	0.41	14	3	1	0.86	0.25	7	9	3	0.61	0.49	0.41
YA5ACA1702	6	5	6	0.50	0.52	18	2	0	0.95	0.10	12	8	0	0.80	0.33	16	0	0	1.00	0.00	0.24
YA5ACA1696	17	3	0	0.93	0.14	20	0	0	1.00	0.00	13	6	0	0.84	0.27	20	0	0	1.00	0.00	0.10
YA5ACA1693	4	5	3	0.54	0.52	1	8	6	0.33	0.46	0	13	5	0.36	0.47	2	1	0	0.83	0.33	0.45
YA5ACA1684	1	14	4	0.42	0.50	0	2	18	0.05	0.10	1	5	14	0.18	0.30	1	3	15	0.13	0.23	0.28
YA5ACA1721	0	3	17	0.08	0.14	0	6	13	0.16	0.27	0	11	8	0.29	0.42	0	3	17	0.08	0.14	0.25
YA5ACA1672	1	13	5	0.39	0.49	6	10	3	0.58	0.50	5	12	2	0.58	0.50	13	7	0	0.83	0.30	0.45
YA5ACA1648	1	6	13	0.20	0.33	3	7	9	0.34	0.46	14	5	0	0.87	0.23	5	9	4	0.53	0.51	0.38
YA5ACA1622	8	8	4	0.60	0.49	17	3	0	0.93	0.14	8	6	5	0.58	0.50	8	7	5	0.58	0.50	0.41
YA5ACA1616	0	1	18	0.03	0.05	0	2	14	0.06	0.12	0	1	14	0.03	0.07	0	1	12	0.04	0.08	0.08
YA5ACA1650	4	11	5	0.48	0.51	5	5	10	0.38	0.48	12	7	1	0.78	0.36	7	7	5	0.55	0.51	0.46
YA5ACA1653	0	2	18	0.05	0.10	0	0	20	0.00	0.00	0	0	20	0.00	0.00	0	0	20	0.00	0.00	0.02
YA5ACA1592	6	8	2	0.63	0.48	12	6	3	0.71	0.42	9	9	2	0.68	0.45	12	4	1	0.82	0.30	0.41
YA5ACA1667	8	12	0	0.70	0.43	20	0	0	1.00	0.00	20	0	0	1.00	0.00	20	0	0	1.00	0.00	0.11
YA5ACA1611	2	4	13	0.21	0.34	10	8	1	0.74	0.40	7	8	3	0.61	0.49	17	0	0	1.00	0.00	0.31
Ya5NBC22	3	15	1	0.55	0.51	4	14	0	0.61	0.49	1	16	1	0.50	0.51	19	1	0	0.98	0.05	0.39
Ya5NBC35	9	10	1	0.70	0.43	5	12	2	0.58	0.50	8	12	0	0.70	0.43	7	13	0	0.68	0.45	0.45
Ya5NBC96	17	2	0	0.95	0.10	9	5	3	0.68	0.45	6	12	0	0.67	0.46	16	3	0	0.92	0.15	0.29
Ya5NBC182	2	9	9	0.33	0.45	9	8	0	0.76	0.37	5	6	7	0.44	0.51	1	10	3	0.43	0.51	0.46
Ya5NBC201	6	6	5	0.53	0.51	4	7	6	0.44	0.51	16	3	0	0.92	0.15	8	7	2	0.68	0.45	0.41
Ya5NBC210	0	4	15	0.11	0.19	0	1	15	0.03	0.06	0	4	16	0.10	0.18	0	4	12	0.13	0.23	0.17
Ya5NBC216	5	7	5	0.50	0.52	6	8	5	0.53	0.51	7	12	0	0.68	0.44	0	0	10	0.00	0.00	0.37
Ya5NBC354	0	2	16	0.06	0.11	2	6	10	0.28	0.41	10	4	5	0.63	0.48	2	4	9	0.27	0.40	0.35
Ya5NBC361	0	9	10	0.24	0.37	2	11	5	0.42	0.50	0	5	12	0.15	0.26	3	3	7	0.35	0.47	0.40
Ya5NBC212	16	1	0	0.97	0.06	20	0	0	1.00	0.00	20	0	0	1.00	0.00	18	0	0	1.00	0.00	0.01
Ya5NBC28	0	0	20	0.00	0.00	0	0	20	0.00	0.00	0	0	20	0.00	0.00	0	0	20	0.00	0.00	0.00
Ya5NBC38	0	0	16	0.00	0.00	0	0	15	0.00	0.00	0	0	20	0.00	0.00	0	0	18	0.00	0.00	0.00
Ya5NBC194	0	0	20	0.00	0.00	0	0	20	0.00	0.00	0	0	20	0.00	0.00	0	0	20	0.00	0.00	0.00
Ya5NBC204	0	0	19	0.00	0.00	0	0	17	0.00	0.00	0	0	17	0.00	0.00	0	0	15	0.00	0.00	0.00
Ya5NBC203	0	0	20	0.00	0.00	0	0	20	0.00	0.00	0	0	20	0.00	0.00	0	0	20	0.00	0.00	0.00
Ya5NBC214	0	0	20	0.00	0.00	0	0	20	0.00	0.00	0	5	15	0.13	0.22	0	0	19	0.00	0.00	0.06
Ya5JW451	15	1	2	0.86	0.25	12	4	3	0.74	0.40	17	2	0	0.95	0.10	14	1	1	0.91	0.18	0.23
Ya5JW495	8	2	2	0.75	0.39	9	2	2	0.77	0.37	12	2	2	0.81	0.31	12	1	2	0.83	0.29	0.34
Ya5JW505	6	4	6	0.50	0.52	5	5	7	0.44	0.51	9	6	4	0.63	0.48	10	1	6	0.62	0.49	0.50
Ya5JW524	5	5	4	0.54	0.52	1	5	12	0.19	0.32	9	5	6	0.58	0.50	4	6	3	0.54	0.52	0.46
Ya5JW539	1	0	9	0.10	0.19	1	0	15	0.06	0.12	1	2	7	0.20	0.34	0	0	12	0.00	0.00	0.16

CHROMOSOME 8

YA5ACA1798	0	7	13	0.18	0.30	0	0	20	0.00	0.00	0	3	17	0.08	0.14	0	3	17	0.08	0.14	0.15
YA5ACA1805	19	1	0	0.98	0.05	19	1	0	0.98	0.05	20	0	0	1.00	0.00	20	0	0	1.00	0.00	0.03
YA5ACA1806	19	1	0	0.98	0.05	19	1	0	0.98	0.05	20	0	0	1.00	0.00	20	0	0	1.00	0.00	0.03
YA5ACA1785	1	4	13	0.17	0.29	0	0	20	0.00	0.00	1	0	19	0.05	0.10	1	0	19	0.05	0.10	0.12
YA5ACA1793	19	1	0	0.98	0.05	19	1	0	0.98	0.05	20	0	0	1.00	0.00	20	0	0	1.00	0.00	0.03
YA5ACA1766	7	6	7	0.50	0.51	13	7	0	0.83	0.30	9	11	0	0.73	0.41	12	8	0	0.80	0.33	0.39
YA5ACA1770	14	4	0	0.89	0.20	12	5	2	0.76	0.37	19	1	0	0.98	0.05	16	3	1	0.88	0.22	0.21
YA5ACA1767	0	3	16	0.08	0.15	0	6	13	0.16	0.27	1	9	8	0.31	0.44	2	11	6	0.39	0.49	0.34
YA5ACA1737	1	2	17	0.10	0.18	4	10	6	0.45	0.51	4	8	6	0.44	0.51	3	14	3	0.50	0.51	0.43
YA5ACA1736	1	7	12	0.23	0.36	0	11	9	0.28	0.41	0	5	14	0.13	0.23	4	6	9	0.37	0.48	0.37

(table cont.)

CHROMOSOME 9																					
YA5ACA1878	7	10	2	0.63	0.48	9	7	3	0.66	0.46	14	2	3	0.79	0.34	15	3	2	0.83	0.30	0.39
YA5ACA1877	0	7	10	0.21	0.34	0	0	16	0.00	0.00	0	0	17	0.00	0.00	0	0	9	0.00	0.00	0.08
YA5ACA1841	0	6	14	0.15	0.26	0	4	16	0.10	0.18	0	0	19	0.00	0.00	0	7	12	0.18	0.31	0.19
Ya5NBC184	0	0	20	0.00	0.00	0	0	18	0.00	0.00	0	0	20	0.00	0.00	0	0	19	0.00	0.00	0.00
YA5ACA1861	7	0	1	0.88	0.23	5	0	2	0.71	0.44	3	4	5	0.42	0.51	7	2	0	0.89	0.21	0.35
YA5ACA1831	0	0	19	0.00	0.00	0	0	18	0.00	0.00	0	0	19	0.00	0.00	0	0	19	0.00	0.00	0.00
CHROMOSOME 10																					
Ya5 541	1	0	16	0.06	0.11	2	0	17	0.11	0.19	11	0	9	0.55	0.51	2	0	16	0.11	0.20	0.25
YA5AC1925	5	12	1	0.61	0.49	12	2	0	0.93	0.14	12	3	0	0.90	0.19	11	2	3	0.75	0.39	0.30
YA5AC1926	15	1	2	0.86	0.25	18	0	0	1.00	0.00	20	0	0	1.00	0.00	18	1	0	0.97	0.05	0.07
YA5AC1939	0	0	20	0.00	0.00	0	3	17	0.08	0.14	0	6	14	0.15	0.26	1	4	15	0.15	0.26	0.17
YA5AC1952	8	7	5	0.58	0.50	0	7	13	0.18	0.30	5	6	6	0.47	0.51	2	9	6	0.38	0.49	0.45
YA5AC1960	3	10	7	0.40	0.49	12	5	3	0.73	0.41	6	10	4	0.55	0.51	8	8	4	0.60	0.49	0.48
YA5AC1972	10	3	4	0.68	0.45	2	4	14	0.20	0.33	4	12	4	0.50	0.51	5	5	2	0.63	0.49	0.45
YA5AC1975	18	2	0	0.95	0.10	17	3	0	0.93	0.14	20	0	0	1.00	0.00	20	0	0	1.00	0.00	0.06
YA5AC1980	8	1	1	0.85	0.27	13	7	0	0.83	0.30	14	5	1	0.83	0.30	15	5	0	0.88	0.22	0.27
YA5AC1982	0	9	11	0.23	0.36	12	5	3	0.73	0.41	0	12	8	0.30	0.43	0	6	14	0.15	0.26	0.36
YA5AC1986	9	9	2	0.68	0.45	16	3	0	0.92	0.15	13	5	2	0.78	0.36	13	6	1	0.80	0.33	0.32
YA5AC1988	9	6	2	0.71	0.43	13	6	1	0.80	0.33	18	2	0	0.95	0.10	17	2	1	0.90	0.18	0.26
YA5AC1997	17	2	1	0.90	0.18	19	1	0	0.98	0.05	13	5	2	0.78	0.36	8	9	3	0.63	0.48	0.27
CHROMOSOME 11																					
Ya5NBC27	0	5	14	0.13	0.23	0	8	11	0.21	0.34	2	7	9	0.31	0.44	2	7	10	0.29	0.42	0.36
Ya5NBC135	0	1	18	0.03	0.05	0	0	20	0.00	0.00	0	0	20	0.00	0.00	0	0	17	0.00	0.00	0.01
YA5AC2013	5	9	4	0.53	0.51	6	6	8	0.45	0.51	7	10	3	0.60	0.49	10	10	0	0.75	0.38	0.47
YA5AC2019	15	3	0	0.92	0.16	7	7	5	0.55	0.51	20	0	0	1.00	0.00	14	6	0	0.85	0.26	0.23
YA5AC2035	10	8	1	0.74	0.40	20	0	0	1.00	0.00	20	0	0	1.00	0.00	20	0	0	1.00	0.00	0.10
YA5AC2045	0	8	12	0.20	0.33	0	1	18	0.03	0.05	0	5	12	0.15	0.26	0	9	11	0.23	0.36	0.25
YA5AC2050	8	9	2	0.66	0.46	17	2	1	0.90	0.18	5	8	5	0.50	0.51	16	3	1	0.88	0.22	0.35
YA5AC2084	15	1	0	0.97	0.06	20	0	0	1.00	0.00	18	0	0	1.00	0.00	18	0	0	1.00	0.00	0.02
YA5AC2095	11	8	1	0.75	0.38	2	13	4	0.45	0.51	10	8	2	0.70	0.43	3	9	6	0.42	0.50	0.46
YA5AC2102	9	6	0	0.80	0.33	11	0	0	1.00	0.00	7	4	0	0.82	0.31	6	0	1	0.86	0.26	0.23
YA5AC2105	8	7	3	0.64	0.47	4	12	3	0.53	0.51	4	8	7	0.42	0.50	7	11	2	0.63	0.48	0.49
YA5AC2122	16	2	2	0.85	0.26	3	8	5	0.44	0.51	11	9	0	0.78	0.36	2	8	10	0.30	0.43	0.39
CHROMOSOME 12																					
Ya5 518	19	1	0	0.98	0.05	20	0	0	1.00	0.00	20	0	0	1.00	0.00	20	0	0	1.00	0.00	0.01
YA5AC2130	5	7	8	0.43	0.50	10	6	4	0.65	0.47	8	8	4	0.60	0.49	3	8	7	0.39	0.49	0.49
YA5AC2140	16	4	0	0.90	0.18	8	11	1	0.68	0.45	9	9	2	0.68	0.45	12	7	1	0.78	0.36	0.36
YA5AC2145	0	4	16	0.10	0.18	4	2	9	0.33	0.46	0	6	14	0.15	0.26	4	3	5	0.46	0.52	0.36
YA5AC2169	15	4	0	0.89	0.19	16	3	0	0.92	0.15	17	3	0	0.93	0.14	16	4	0	0.90	0.18	0.17
YA5AC2181	15	5	0	0.88	0.22	18	0	0	1.00	0.00	20	0	0	1.00	0.00	19	1	0	0.98	0.05	0.07
YA5AC2182	9	3	2	0.75	0.39	18	2	0	0.95	0.10	16	4	0	0.90	0.18	17	3	0	0.93	0.14	0.20
YA5AC2205	6	8	6	0.50	0.51	18	2	0	0.95	0.10	6	13	0	0.66	0.46	10	8	0	0.78	0.36	0.36
YA5AC2215	0	2	18	0.05	0.10	0	0	20	0.00	0.00	0	0	20	0.00	0.00	0	3	17	0.08	0.14	0.06
YA5AC2221	18	2	0	0.95	0.10	20	0	0	1.00	0.00	20	0	0	1.00	0.00	20	0	0	1.00	0.00	0.02
YA5AC2222	8	2	1	0.82	0.31	3	2	1	0.67	0.48	3	2	0	0.80	0.36	11	5	0	0.84	0.27	0.36
YA5AC2227	10	5	4	0.66	0.46	6	11	0	0.68	0.45	4	11	2	0.56	0.51	5	11	2	0.58	0.50	0.48

(table cont.)

CHROMOSOME 13																					
Ya5 545	8	2	5	0.60	0.50	11	2	4	0.71	0.43	8	4	8	0.50	0.51	9	1	3	0.73	0.41	0.46
Ya5 552	0	5	15	0.13	0.22	0	1	19	0.03	0.05	0	0	20	0.00	0.00	0	1	18	0.03	0.05	0.08
YA5AC2247	8	8	4	0.60	0.49	11	7	2	0.73	0.41	12	7	1	0.78	0.36	12	6	1	0.79	0.34	0.40
YA5AC2259	1	8	11	0.25	0.38	0	9	11	0.23	0.36	0	7	13	0.18	0.30	0	4	16	0.10	0.18	0.31
YA5AC2265	4	8	6	0.44	0.51	9	7	3	0.66	0.46	12	6	1	0.79	0.34	9	10	1	0.70	0.43	0.44
YA5AC2268	0	7	13	0.18	0.30	9	9	2	0.68	0.45	3	14	3	0.50	0.51	6	8	6	0.50	0.51	0.44
YA5AC2272	5	10	5	0.50	0.51	3	11	6	0.43	0.50	6	12	2	0.60	0.49	3	12	5	0.45	0.51	0.50
YA5AC2278	7	9	4	0.58	0.50	0	14	6	0.35	0.47	11	7	2	0.73	0.41	10	7	3	0.68	0.45	0.46
YA5AC2282	3	6	11	0.30	0.43	16	4	0	0.90	0.18	16	2	2	0.85	0.26	15	5	0	0.88	0.22	0.28
YA5AC2294	1	11	8	0.33	0.45	1	7	12	0.23	0.36	0	8	12	0.20	0.33	0	9	11	0.23	0.36	0.37
YA5AC2296	8	8	2	0.67	0.46	20	0	0	1.00	0.00	20	0	0	1.00	0.00	20	0	0	1.00	0.00	0.11
YA5AC2300	0	5	15	0.13	0.22	0	6	14	0.15	0.26	0	3	17	0.08	0.14	0	2	18	0.05	0.10	0.18
YA5AC2305	2	7	11	0.28	0.41	0	1	18	0.03	0.05	5	12	3	0.55	0.51	6	7	5	0.53	0.51	0.37
YA5AC2312	0	3	17	0.08	0.14	0	0	20	0.00	0.00	0	0	20	0.00	0.00	0	0	19	0.00	0.00	0.04
YA5AC2323	0	7	13	0.18	0.30	1	9	10	0.28	0.41	4	9	7	0.43	0.50	4	7	8	0.39	0.49	0.42
YA5AC2330	9	9	1	0.71	0.42	20	0	0	1.00	0.00	20	0	0	1.00	0.00	20	0	0	1.00	0.00	0.11
YA5AC2333	15	4	1	0.85	0.26	16	4	0	0.90	0.18	16	4	0	0.90	0.18	19	1	0	0.98	0.05	0.17
YA5AC2336	0	5	9	0.18	0.30	0	0	20	0.00	0.00	0	0	20	0.00	0.00	0	0	20	0.00	0.00	0.08
CHROMOSOME 14																					
Ya5NBC333	5	5	9	0.39	0.49	4	7	8	0.39	0.49	3	8	8	0.37	0.48	5	3	5	0.50	0.52	0.49
Ya5 533	0	0	20	0.00	0.00	0	0	20	0.00	0.00	0	0	20	0.00	0.00	0	0	20	0.00	0.00	0.00
Ya5JW580	2	7	7	0.34	0.47	2	5	12	0.24	0.37	0	5	15	0.13	0.22	2	9	4	0.43	0.51	0.39
YA5AC2360	6	7	6	0.50	0.51	4	13	2	0.55	0.51	7	7	6	0.53	0.51	4	7	9	0.38	0.48	0.50
YA5AC2366	4	10	6	0.45	0.51	12	6	1	0.79	0.34	17	3	0	0.93	0.14	16	4	0	0.90	0.18	0.29
YA5AC2368	8	10	2	0.65	0.47	13	7	0	0.83	0.30	14	6	0	0.85	0.26	18	2	0	0.95	0.10	0.28
YA5AC2369	9	11	0	0.73	0.41	17	3	0	0.93	0.14	12	5	3	0.73	0.41	14	5	1	0.83	0.30	0.31
YA5AC2370	13	5	0	0.86	0.25	20	0	0	1.00	0.00	20	0	0	1.00	0.00	20	0	0	1.00	0.00	0.06
YA5AC2376	16	4	0	0.90	0.18	15	4	1	0.85	0.26	19	0	0	1.00	0.00	13	0	0	1.00	0.00	0.11
YA5AC2380	12	6	2	0.75	0.38	18	2	0	0.95	0.10	20	0	0	1.00	0.00	17	3	0	0.93	0.14	0.16
YA5AC2388	5	7	8	0.43	0.50	7	11	2	0.63	0.48	2	16	2	0.50	0.51	10	8	1	0.74	0.40	0.47
YA5AC2389	13	6	0	0.84	0.27	6	1	1	0.81	0.33	12	7	0	0.82	0.31	12	3	1	0.84	0.27	0.29
YA5AC2390	4	13	1	0.58	0.50	6	10	3	0.58	0.50	11	9	0	0.78	0.36	5	12	3	0.55	0.51	0.47
YA5AC2404	14	6	0	0.85	0.26	17	0	0	1.00	0.00	20	0	0	1.00	0.00	20	0	0	1.00	0.00	0.07
YA5AC2408	0	2	18	0.05	0.10	0	0	20	0.00	0.00	0	2	18	0.05	0.10	0	0	20	0.00	0.00	0.05
YA5AC2409	0	0	20	0.00	0.00	0	0	17	0.00	0.00	0	0	12	0.00	0.00	0	0	15	0.00	0.00	0.00
YA5AC2410	17	2	1	0.90	0.18	20	0	0	1.00	0.00	19	1	1	0.93	0.14	20	0	0	1.00	0.00	0.08
CHROMOSOME 15																					
YA5AC2434	0	2	18	0.05	0.10	0	1	19	0.03	0.05	0	5	15	0.13	0.22	0	2	18	0.05	0.10	0.12
YA5AC2456	4	15	1	0.58	0.50	14	4	0	0.89	0.20	15	3	0	0.92	0.16	15	0	0	1.00	0.00	0.22
YA5AC2458	4	9	5	0.47	0.51	0	0	18	0.00	0.00	1	4	12	0.18	0.30	3	15	0	0.58	0.50	0.33
YA5AC2465	0	0	19	0.00	0.00	0	0	17	0.00	0.00	0	0	18	0.00	0.00	0	0	19	0.00	0.00	0.00
CHROMOSOME 16																					
Ya5NBC57	10	1	2	0.81	0.32	4	8	3	0.53	0.51	13	2	1	0.88	0.23	9	1	1	0.86	0.25	0.33
Ya5 453[2]	0	17	3	0.43	0.50	0	16	3	0.42	0.50	0	10	10	0.25	0.38	1	11	7	0.34	0.46	0.46
Ya5 464	13	2	3	0.78	0.36	17	0	0	1.00	0.00	11	3	4	0.69	0.44	14	2	2	0.83	0.29	0.27
Ya5 531	2	0	5	0.29	0.44	15	0	0	1.00	0.00	19	0	0	1.00	0.00	3	0	1	0.75	0.43	0.22

(table cont.)

YA5AC2480																				
YA5AC2480	0	19	1	0.48	0.51	0	16	4	0.40	0.49	0	18	2	0.45	0.51	0	14	5	0.37	0.48	0.50
YA5AC2487	0	0	20	0.00	0.00	0	0	20	0.00	0.00	0	0	20	0.00	0.00	0	0	20	0.00	0.00	0.00
YA5AC2525	0	0	20	0.00	0.00	1	5	13	0.18	0.31	0	0	18	0.00	0.00	2	2	13	0.18	0.30	0.15
CHROMOSOME 17																				
Ya5NBC102	3	2	13	0.22	0.36	0	0	6	0.00	0.00	3	4	12	0.26	0.40	1	1	13	0.10	0.19	0.24
Ya5NBC120	7	11	0	0.69	0.44	15	4	0	0.89	0.19	8	12	0	0.70	0.43	14	5	0	0.87	0.23	0.32
Ya5NBC157	20	0	0	1.00	0.00	20	0	0	1.00	0.00	20	0	0	1.00	0.00	15	0	1	0.94	0.12	0.03
Ya5NBC160	2	7	9	0.31	0.44	0	0	19	0.00	0.00	0	0	19	0.00	0.00	0	4	12	0.13	0.23	0.17
Ya5 421	7	0	10	0.41	0.50	5	0	11	0.31	0.44	6	1	11	0.36	0.47	4	2	10	0.31	0.44	0.47
Ya5 435	2	4	14	0.20	0.33	6	10	2	0.61	0.49	3	10	7	0.40	0.49	4	0	0	1.00	0.00	0.33
Ya5 454	0	4	16	0.10	0.18	3	5	12	0.28	0.41	4	5	11	0.33	0.45	0	5	12	0.15	0.26	0.33
YA5AC2539	7	3	7	0.50	0.52	7	4	7	0.50	0.51	6	3	7	0.47	0.51	2	5	4	0.41	0.51	0.51
YA5AC2571	12	7	1	0.78	0.36	14	6	0	0.85	0.26	17	3	0	0.93	0.14	14	6	0	0.85	0.26	0.26
YA5AC2577	4	13	3	0.53	0.51	7	10	3	0.60	0.49	4	8	7	0.42	0.50	5	8	7	0.45	0.51	0.50
CHROMOSOME 18																				
Ya5 432	16	1	1	0.92	0.16	20	0	0	1.00	0.00	20	0	0	1.00	0.00	20	0	0	1.00	0.00	0.04
YA5AC2584	5	11	3	0.55	0.51	9	10	1	0.70	0.43	5	7	7	0.45	0.51	8	8	2	0.67	0.46	0.48
YA5AC2585	0	0	17	0.00	0.00	0	0	7	0.00	0.00	0	0	18	0.00	0.00	0	0	12	0.00	0.00	0.00
YA5AC2596	0	7	12	0.18	0.31	0	0	19	0.00	0.00	0	0	19	0.00	0.00	0	0	20	0.00	0.00	0.08
YA5AC2608	0	0	20	0.00	0.00	0	0	9	0.00	0.00	0	0	8	0.00	0.00	0	0	7	0.00	0.00	0.00
YA5AC2613	14	6	0	0.85	0.26	20	0	0	1.00	0.26	20	0	0	1.00	0.00	20	0	0	1.00	0.00	0.13
YA5AC2617	0	2	18	0.05	0.18	0	0	20	0.00	0.10	0	0	20	0.00	0.00	0	2	18	0.05	0.00	0.07
CHROMOSOME 19																				
Ya5NBC150	17	0	0	1.00	0.00	4	5	9	0.36	0.47	19	0	1	0.95	0.10	17	0	1	0.94	0.11	0.17
Ya5NBC349	19	1	0	0.98	0.05	14	0	0	1.00	0.00	18	0	0	1.00	0.00	12	0	2	0.86	0.25	0.08
Ya5 416	0	0	20	0.00	0.00	0	0	20	0.00	0.00	0	0	20	0.00	0.00	1	13	4	0.42	0.50	0.13
YA5AC2662	10	9	0	0.76	0.37	8	4	0	0.83	0.29	18	2	0	0.95	0.10	10	9	0	0.76	0.37	0.28
YA5AC2670	6	3	8	0.44	0.51	0	0	15	0.00	0.00	0	0	13	0.00	0.00	1	2	7	0.20	0.34	0.21
CHROMOSOME 20																				
Ya5NBC45	7	7	2	0.66	0.47	19	0	0	1.00	0.00	17	0	0	1.00	0.00	8	3	0	0.86	0.25	0.18
Ya5NBC148	7	6	6	0.53	0.51	2	6	12	0.25	0.38	0	0	20	0.00	0.00	0	0	17	0.00	0.00	0.22
Ya5 542	0	0	20	0.00	0.00	0	0	20	0.00	0.00	0	0	19	0.00	0.00	0	0	12	0.00	0.00	0.00
Ya5 550	0	0	18	0.00	0.00	0	0	20	0.00	0.00	4	3	13	0.28	0.41	0	0	18	0.00	0.00	0.10
Ya5 563	0	0	20	0.00	0.00	0	0	20	0.00	0.00	0	0	20	0.00	0.00	0	0	20	0.00	0.00	0.00
Ya5 564[2]	5	10	5	0.50	0.51	20	0	0	1.00	0.00	18	2	0	0.95	0.10	15	3	0	0.92	0.16	0.19
Ya5 567[2]	6	9	5	0.53	0.51	1	1	18	0.08	0.14	1	7	12	0.23	0.36	1	10	8	0.32	0.44	0.36
YA5AC2698	18	2	0	0.95	0.10	17	0	0	1.00	0.00	12	1	1	0.89	0.20	10	0	0	1.00	0.00	0.07
YA5AC2704	3	5	1	0.61	0.50	3	2	0	0.80	0.36	13	2	3	0.78	0.36	12	2	3	0.76	0.37	0.40
YA5AC2706	2	5	0	0.64	0.49	11	0	0	1.00	0.00	6	1	1	0.81	0.33	0	4	16	0.10	0.18	0.25
YA5AC2709	2	2	15	0.16	0.27	2	6	6	0.36	0.48	0	4	7	0.18	0.31	3	8	9	0.35	0.47	0.38
YA5AC2715	0	2	17	0.05	0.10	2	2	7	0.27	0.42	0	0	7	0.00	0.00	3	3	9	0.30	0.43	0.24
CHROMOSOME 21																				
Ya5NBC24	0	0	20	0.00	0.00	0	0	20	0.00	0.00	0	0	20	0.00	0.00	0	0	20	0.00	0.00	0.00
Ya5NBC351	3	12	3	0.50	0.51	7	9	3	0.61	0.49	13	3	3	0.76	0.37	6	10	5	0.52	0.51	0.47
Ya5 448	0	0	20	0.00	0.00	0	0	10	0.00	0.00	0	0	20	0.00	0.00	0	0	19	0.00	0.00	0.00

(table cont.)

YA5AC2731	15	5	0	0.88	0.22	19	0	0	1.00	0.00	17	0	0	1.00	0.00	18	0	0	1.00	0.00	0.06
CHROMOSOME 22																					
Ya5NBC109	7	11	1	0.66	0.46	7	11	2	0.63	0.48	5	13	1	0.61	0.49	7	8	4	0.58	0.50	0.48
Ya5NBC221	5	7	4	0.53	0.51	9	5	3	0.68	0.45	16	0	1	0.94	0.11	13	2	0	0.93	0.13	0.30
Ya5NBC223	0	0	20	0.00	0.00	0	0	20	0.00	0.00	0	0	20	0.00	0.00	0	0	19	0.00	0.00	0.00

1. f represents the frequency of the element.
2. This is unbiased heterozygosity: H=(2*sample size * (1-sum freq of homozygotes))/(2*sample size – 1).
3. Average heterozygosity is the average heterozygosity for all populations.
4. Asian and Alaskan Native samples were used interchangeably as a geographically unique human population

VITA

Anthony Otieno was born in 1973 in Nairobi, Kenya, to Adonijah and Florence Otieno. He graduated with a Bachelor of Science degree in biochemistry from the University of Nairobi in December 1997. He joined the Department of Biological Sciences in Louisiana State University in January 1999. He is married to Faith Atieno and they are the proud parents of Marc Owiti. Mr. Otieno will graduate with the degree of Doctor of Philosophy in biochemistry from Louisiana State University in May 2005.